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Signaling Pathways in Mammary Tumorigenesis

PRINCIPAL INVESTIGATOR: William J. Muller, Ph.D.

CONTRACTING ORGANIZATION: McMaster University  
Hamilton, Ontario L8N 3Z5 Canada

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7. PERFORMING ORGANIZATION NAME(S) AND ADDRESS(ES)  McMaster University Hamilton, Ontario L8N 3Z5 Canada  E-Mail: mullerw@mcmaster.ca		8. PERFORMING ORGANIZATION REPORT NUMBER		
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## INTRODUCTION

The research objective outlined in the original proposal was to elucidate the roles of the phosphatidylinositol 3' kinase (PI3K) and its downstream signaling partners in the induction of mammary tumors. The work is based on observations in transgenic mice that overexpress a mutant Polyomavirus middle T (PyV mT) oncogene that is decoupled from the PI3K signaling pathway (MTY315/322F) under control of the mouse mammary tumor virus (MMTV) long terminal repeat (LTR) in the mammary gland. In contrast to transgenic mice expressing wildtype PyV mT which rapidly develop multifocal metastatic mammary tumors, transgenic strains expressing MTY315/322F develop extensive mammary epithelial hyperplasias that are highly apoptotic<sup>1,2</sup>. Although mammary tumors do eventually develop in this strain, they are focal and form with considerably longer latency than in the wildtype strain. Furthermore, in contrast to the 100% metastasis observed in the wildtype strain, a greatly reduced number of the MMTV-MTY315/322F tumors metastasize to the lung. Based on these observations, we are directly assessing the importance of activation of the PI3K and its downstream targets such as the Akt serine/threonine kinase and the small GTPase Rac<sup>3,4</sup> in mammary tumorigenesis and metastasis through the use of transgenic mice expressing constitutively active forms of PI3K or Akt. Although we have not at this time succeeded in deriving mice expressing constitutively active PI3K we have generated mice that express constitutively active Akt (Akt-DD) in the mammary gland. While expression of Akt-DD interferes with the apoptotic process of normal mammary gland involution, tumors were not observed in these strains. However, co-expression of Akt-DD with MTY315/322F resulted in a dramatic acceleration of mammary tumorigenesis correlated with reduced apoptotic cell death. Importantly, we did not observe an associated restoration of wildtype metastasis levels in the bi-transgenic strain (Appendix1). Furthermore, preliminary results indicate that activated Akt may contribute to ErbB-2 tumorigenesis, as co-expression of activated Akt and an activated ErbB-2 in the mammary gland greatly increases mammary tumor formation. Taken together these observations indicate that activation of Akt can contribute to tumor progression by providing an important cell survival signal but does not promote metastatic progression. It is hoped that the knowledge generated by these studies will enhance our understanding of the genetic process of breast cancer yielding new targets for therapy and enable better assessments of risk factors in human breast cancer progression.

## RESEARCH ACCOMPLISHMENTS

### 1) Final characterization of the MMTV/activated Akt transgenics.

One goal of the proposal was to further characterize the developmental effects of the activated Akt transgene (Akt-DD) on the mammary glands of the MMTV-Akt7 strain. Akt-DD had no detectable effect on virgin mammary gland with female virgin Akt transgenic mice having yet to develop mammary tumors after a year of observation. This observation is now further supported by the observation that multiparous Akt females, which would have undergone multiple periods of high transgene expression, have also failed to exhibit tumors. Given Akt's role in promoting cellular survival, we investigated whether Akt-DD could affect the apoptotic process of mammary gland involution. Mammary glands from wild type and activated Akt strains were examined at 1, 3 and 7-days post-parturition. In contrast to wild type control animals which exhibited extensive involution at 1 and 3-days post-parturition (Appendix 1, Fig. 3A,C,E,G), the Akt animals displayed a dramatic defect in mammary gland involution (Appendix 1, Fig. 3B,D,F,H). However, the Akt mammary glands eventually underwent full involution at 7-days post-parturition (data not shown). TUNEL analyses were conducted on involuting mammary

epithelium derived from FVB and Akt strains (Appendix 1, Fig. 4) and the results revealed that mammary glands derived from the involuting FVB glands exhibited elevated levels of apoptotic cell death relative to mammary epithelium of the Akt strains (compare Appendix 1, Fig. 4A to 4B). Taken together, these observations argue that activation of Akt can interfere with normal mammary gland involution by attenuating apoptotic death in the involuting mammary gland.

## **2) Characterization of the bi-transgenics generated by interbreeding the MMTV/activated Akt, MMTV/-MTY315/322F and MMTV/activated ErbB-2 strains.**

Another goal of the original research was to explore the contribution of Akt activation in PyV mT and ErbB-2 mediated mammary tumorigenesis. As stated in the original proposal, to explore whether Akt-DD expression could complement the defect in tumorigenesis exhibited by transgenic mice expressing the MTY315/322F bi-transgenics expressing both Akt-DD and MTY315/322F were derived and monitored for tumor formation. The results of these analyses revealed that bi-transgenic mice developed multifocal tumors with shorter latency than observed in the MTY315/322F strain. In agreement with these analyses these lesions could be subcutaneously transplanted into syngeneic recipients. To confirm that bi-transgenics expressing MTY315/322F and Akt-DD exhibited elevated Akt kinase activity, we examined the total Akt kinase activity against a peptide substrate in virgin FVB, MTY315/322F and bi-transgenic mammary glands. These studies revealed an approximately five-fold increase in the total Akt kinase activity in the bi-transgenic mammary glands as compared to those of MTY315/322F transgenics (Appendix 1, Fig. 6A). The minimal increases in endogenous Akt phosphorylation (Appendix 1, Fig. 6B) would suggest that the majority of the Akt kinase activity is derived from the activated mutant.

As the mammary epithelial hyperplasias associated with the mutant PyV mT strains possess elevated levels of apoptotic cell death, we measured the degree of apoptotic cell death in mammary glands derived from the bi-transgenic mice. The results revealed that mammary epithelial expression of Akt-DD resulted in a dramatic repression of the high rates of apoptotic cell death in MTY315/322F tissue (Appendix 1, Fig. 6B). Taken together, these observations argue that the dramatic acceleration of mammary tumorigenesis exhibited by these strains is due to the ability of activated Akt to suppress the elevated apoptotic cell death displayed by mutant PyV mT mammary epithelium.

To further explore the molecular basis for the observed cooperative interaction between Akt-DD and MTY315/322F, we assessed the status of some of the known targets of Akt, including BAD<sup>5</sup>, I-kappa-B<sup>6</sup> and the FKHR forkhead transcription factor<sup>7</sup>. No significant differences in either BAD-Ser136 phosphorylation or I-kappa\_B levels were observed between the various transgenic strains (data not shown). However immunoblot analysis with phospho-specific antisera to serine 256 of FKHR-1 revealed that the mammary tissue samples derived from bi-transgenic animals expressed elevated levels of phosphorylated FKHR protein relative to other control transgenic tissue samples (Appendix 1, Fig. 7A). To further explore this observation we examined the status of p27/Kip1 as forkhead transcription factors have been shown to target expression of the cell cycle regulator p27/Kip1<sup>8,9</sup>. However examination of p27/Kip1 levels by Western blot revealed no apparent decreases in p27/Kip1 levels in the bi-transgenic animals as compared to MTY315/322F and FVB/n controls (Appendix 1, Fig. 7B, third panel).

Another potential target for PI3K/Akt kinase axis is the cell cycle machinery as it has been demonstrated that suppression of the PI3K signaling pathway by the PTEN tumor suppressor results in down regulation of cyclin D1 expression and cell cycle arrest<sup>10</sup>.

Immunoblot analysis revealed that the bi-transgenic tissues co-expressing both Akt-DD and the mutant PyV mT oncogene exhibited dramatically elevated levels of cyclin D1 (Appendix 1, Fig. 7A, third panel). The differences in cyclin D1 protein were not due to increased levels of cyclin D1 transcripts since these samples expressed comparable levels of cyclin D1 transcript (data not shown). A potential mechanism for the increased levels of cyclin D1 was suggested by the ability of Akt and MAP kinases to phosphorylate and inhibit glycogen synthase kinase-3 (GSK3)<sup>11,12</sup>, which has been shown to target cyclin D1 for proteasomal degradation<sup>13</sup>. However, analysis of GSK3 phosphorylation showed no significant increases in the bi-transgenic strain as compared to FVB/n and MTY315/322F controls, once differences in GSK3 levels were accounted for (Appendix 1, Fig. 7B, first and second panels).

The original proposal also outlined experiments to examine the contribution of Akt activation to ErbB-2 mediated mammary tumorigenesis. To pursue these studies, transgenic mice co-expressing Akt-DD and the NDL2-5 activated ErbB-2<sup>14</sup> transgenes have been generated. Preliminary results indicate that activated Akt may contribute to ErbB-2 tumorigenesis, as bi-transgenics show reduced latency of mammary tumor formation (Appendix 2, Fig. 1).

### **The role of Akt signaling axis in metastatic progression**

As noted in the original proposal, simple histological assessment of metastasis is not beyond doubt, as it does not account for differences in tumor kinetics and load amongst the transgenic strains. Therefore we proposed to subcutaneously transplant primary cells from the various transgenic lines into syngeneic FVB/n animals and track tumor growth and metastasis to the lung. Metastasis levels would be quantitated using either Southern or PCR analysis against the transgene. These studies have been initiated and only the final quantitation remains to be completed. Matrigel invasion experiments will also be used to corroborate these *in vivo* studies.

To support these primary tumor cell studies, we have also derived cell lines from mammary tumors derived from bi-transgenics co-expressing Akt-DD and MTY315/322F (Appendix 2, Fig. 2). These cell lines will be used for similar *in vivo* and cell culture experiments as outlined above.

As the small GTPase Rac is a target of PI3K that has been implicated in cell motility signaling<sup>15</sup>, we propose to extend the above studies to study the role of Rac in PyV mT mediated metastasis. To do so, we have derived retroviral vectors expressing activated, dominant negative and wildtype versions of Rac and RhoA as well as activated PI3K and Akt controls. These retroviral vectors also contain an internal ribosome entry site (IRES) following the transgene, which allows the expression the potent selectable marker blastocystin in tandem with the transgene, allowing easy selection of cells expressing the construct. These studies will be initiated in the fall of 2001 under the aegis of different funding agency.

The original proposal also outlined experiments to examine the capacity of PI3K activation to affect mammary tumorigenesis alone and to determine its contribution to PyV mT and ErbB-2 mediated mammary tumorigenesis using transgenic mice expressing activated PI3K in the mammary gland. However, we have been unable to derive transgenic mice that express elevated levels of the activated PI-3K despite the generation of 5 independent transgenic strains (Appendix 2, Figure 3). We are currently deriving more lines to screen for transgene expression using a newly prepared injection fragment. It is anticipated that the mice will be derived before the end of 2001 and characterized in the next year.

## KEY RESEARCH ACCOMPLISHMENTS

- Further characterization of mice expressing activated Akt in the mammary epithelium demonstrating defects in apoptosis during involution.
- Further molecular and biological characterization of mice co-expressing activated Akt and MTY315/322F in the mammary epithelium demonstrating anti-apoptotic effect of the transgene and revealing molecular targets involved in tumor formation.
- Generation of cell lines from mammary tumors derived from bi-transgenics co-expressing activated Akt and MTY315/322F.
- Interbreeding of the MMTV/activated Akt mice with MMTV/activated erbB-2 mice, to assess role of Akt in erbB-2-induced mammary tumorigenesis.

## REPORTABLE OUTCOME

- Manuscript – “Activation of Akt (protein kinase B) in mammary epithelium provides a critical cell survival signal required for tumor progression.” Hutchinson J, Jin J, Cardiff R, Woodgett J, Muller W., *Mol Cell Biol*, 2001 Mar;21(6):2203-12. (see reprint, Appendix 1).
- Manuscript – “Transgenic mouse models of human breast cancer.” Hutchinson, J & Muller W., *Oncogene*, 2000 Dec 11;19(53):6130. (see reprint, Appendix 3)
- Oral presentation - Canadian Breast Cancer Research Initiative, Reasons for Hope Meeting, LeConcorde Hotel, Quebec City, Quebec, May 3-5, 2001 (see abstract, p. 33, Appendix 4)
- Abstract - The Fifth Conference on Signaling in Normal and Cancer Cells, Banff Centre for Conferences, Banff, Alberta, March 2-6, 2001 (see abstract, p. 34, Appendix 4)
- Oral presentation - Oncogene Meeting, Salk Institute, San Diego, California, USA, June 22-25, 2000 (see abstract, p. 35, Appendix 4)

## CONCLUSIONS

Funding for this project was provided in order to assess the roles of the phosphatidylinositol 3' kinase (PI3K) and its downstream signaling partners in the induction of mammary tumors. We have demonstrated that the activation of Akt in the mammary gland can adversely affect mammary gland involution and partially contribute to PyV mT mediated mammary tumorigenesis via its effects on these processes through its effects on cellular apoptosis. Importantly, Akt has these effects on tumorigenesis but does not affect metastasis. These results are directly relevant to the understanding of the molecular mechanisms behind invasive breast cancer, as the overexpression of the PTEN tumor suppressor has been shown to induce apoptosis and cell cycle arrest through Akt-dependent pathways in a breast cancer cell line<sup>16</sup>. Preliminary results with bi-transgenics co-expressing Akt-DD and activated ErbB-2 support the notion that activation of this cell survival pathway may also contribute to mammary tumor progression in ErbB-2 induced tumorigenesis.

Consistent with its role in promoting tumorigenesis, Akt activation resulted in the phosphorylation and inactivation of FKHR, a transcription factor involved in promoting apoptosis<sup>17</sup>. Interestingly, we observed little to no effect on such Akt targets as BAD, I-kappa-B or GSK 3B. These results may reflect the different nature of the tissues and signals involved in these experiments. Furthermore, our finding that the combination of Akt-DD and MTY315/322F resulted in a non-transcriptional upregulation of cyclin D1 suggests that the concerted activation of both cell survival and proliferative signaling pathways may be a common requirement for oncogenic transformation of primary cells.

Another important finding of our DOD funded research program was the observation that

complementation of tumor progression in the MTY315/322F strains was not associated with increase in metastatic invasion. These observations suggest that the signaling requirements necessary for tumorigenesis may be distinct from those required for metastatic invasion. Indeed it is conceivable that other members of the Akt family such as Akt-2 may provide this metastatic signal. Alternatively other downstream targets of the PI3K pathway such as Rac family of GTPase may fulfill this function. Future studies with these transgenic should allow these issues to addressed.

The inability to derive mice expressing activated PI3K in the mammary gland has delayed our ability to fully pursue a portion of the proposed research. Although we have obtained five independent transgenic mice, these strains fail to express the transgene in the mammary epithelium. This may reflect leaky expression of this activated PI3K during embryogenesis leading embryonic lethality. Indeed we have previously demonstrated that MMTV driven expression of Adenoviral E1A results in embryonic lethality.

To circumvent this problem we are currently pursuing *in vivo* transplant studies employing cells transfected with a retrovirus expressing the activated PI3K construct. These studies, should provide answers to the questions posed in the original proposal. In summary, the results of these combined studies has increased our knowledge of the importance of PI3K and Akt in mammary tumorigenesis and metastasis. It is hoped that these results will aid in the assessment of patient's risk level at the time of diagnosis and may be used to assess therapeutic targets for the treatment of breast cancer.

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## **Appendix 1**

Manuscript published in Molecular and Cellular Biology.  
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## Activation of Akt (Protein Kinase B) in Mammary Epithelium Provides a Critical Cell Survival Signal Required for Tumor Progression

JOHN HUTCHINSON,<sup>1</sup> JING JIN,<sup>2</sup> ROBERT D. CARDIFF,<sup>3</sup> JIM R. WOODGETT,<sup>2</sup>  
AND WILLIAM J. MULLER<sup>1\*</sup>

*MOBIX, McMaster University, Hamilton,<sup>1</sup> and Ontario Cancer Institute, Toronto,<sup>2</sup> Ontario, Canada, and  
University of California at Davis, Davis, California<sup>3</sup>*

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Activation of Akt by the phosphatidylinositol 3'-OH kinase (PI3K) results in the inhibition of proapoptotic signals and the promotion of survival signals (L. P. Kane et al., *Curr. Biol.* 9:601–604, 1999; G. J. Kops et al., *Nature* 398:630–634, 1999). Evidence supporting the importance of the PI3K/Akt signaling pathway in tumorigenesis stems from experiments with transgenic mice bearing polyomavirus middle T antigen under the control of the mouse mammary tumor virus long terminal repeat promoter. Mammary epithelium-specific expression of polyomavirus middle T antigen results in the rapid development of multifocal metastatic mammary tumors, whereas transgenic mice expressing a mutant middle T antigen decoupled from the phosphatidylinositol 3'-OH kinase (MTY315/322F) develop extensive mammary gland hyperplasias that are highly apoptotic. To directly assess the role of Akt in mammary epithelial development and tumorigenesis, we generated transgenic mice expressing constitutively active Akt (HAPKB308D473D or Akt-DD). Although expression of Akt-DD interferes with normal mammary gland involution, tumors were not observed in these strains. However, coexpression of Akt-DD with MTY315/322F resulted in a dramatic acceleration of mammary tumorigenesis correlated with reduced apoptotic cell death. Furthermore, coexpression of Akt-DD with MTY315/322F resulted in phosphorylation of the FKHR forkhead transcription factor and translational upregulation of cyclin D1 levels. Importantly, we did not observe an associated restoration of wild-type metastasis levels in the bistransgenic strain. Taken together these observations indicate that activation of Akt can contribute to tumor progression by providing an important cell survival signal but does not promote metastatic progression.

The growth and development of the mammary gland is regulated by a complex set of factors including hormones, cell-substratum interactions, and growth factors and their associated receptors. Activation of growth factor receptors leads to the recruitment of a number of cytoplasmic signaling molecules, including the phosphatidylinositol 3'-OH kinase (PI3K). Recruitment of the PI3K to the cell membrane by these activated growth factors or docking molecules then results in the activation of a number of molecules. PI3K-dependent generation of phosphatidylinositol 3' phosphate provides docking sites for several Pleckstrin homology (PH) domain-harboring molecules including Akt (also known as protein kinase B [PKB]) as well as its upstream kinases, PDK1 and the proposed PDK2 (2, 16). These latter enzymes phosphorylate Akt at threonine 308 and serine 473, respectively, causing full Akt activation (1, 2). Activation of Akt subsequently results in the inhibition of proapoptotic signals from such proteins as BAD (9), caspase 9 (4), and the forkhead transcription factor family (3, 22, 34) and the promotion of survival signals from such proteins as NF- $\kappa$ B (20). Although evidence suggests roles for PI3K and Akt in normal mammary development (15) and tumorigenesis (5, 30, 31, 35), the role of these signaling molecules in these processes remains to be elucidated.

Evidence supporting the importance of the PI3K/Akt signaling pathway in tumorigenesis stems from experiments with transgenic mice bearing polyomavirus (PyV) middle T antigen (mT) under the control of the mouse mammary tumor virus long terminal repeat promoter (MMTV-LTR). The MMTV-LTR is transcriptionally active throughout mammary development, and its transcriptional activity increases during pregnancy (26). Mammary epithelium-specific expression of PyV mT results in the rapid development of multifocal metastatic mammary tumors (18) due to its ability to associate with and activate the Src family kinases, PI3K, and the Shc adapter protein (6, 7, 14). In contrast to the rapid tumor progression observed in transgenic mice carrying the PyV mT oncogene (MT634), transgenic mice expressing a mutant mT decoupled from the PI3K pathway (MMTV/MTY315/322F) develop extensive mammary gland hyperplasias that are highly apoptotic (35). Focal mammary tumors do eventually arise in these strains and are further correlated with upregulation of the ErbB-2 and ErbB-3 growth factor receptors (35). In addition, these tumors show defects in metastatic progression (35).

The defects in tumor progression in the mutant mT strain suggested that Akt may play important roles in tumorigenesis by inhibiting apoptosis and/or promoting metastasis. In this report we show that activation of Akt alone can interfere with the apoptotic process of mammary gland involution and promote tumor progression by providing an important cell survival signal but does not promote metastasis. The dramatic acceleration of tumor progression in these strains was further corre-

\* Corresponding author. Mailing address: MOBIX, McMaster University, 1280 Main St. W., Hamilton, Ontario L8S 4K1, Canada. Phone: (905) 525-9140, ext. 27306. Fax: (905) 521-2955. E-mail: mullerw@mcmaster.ca.

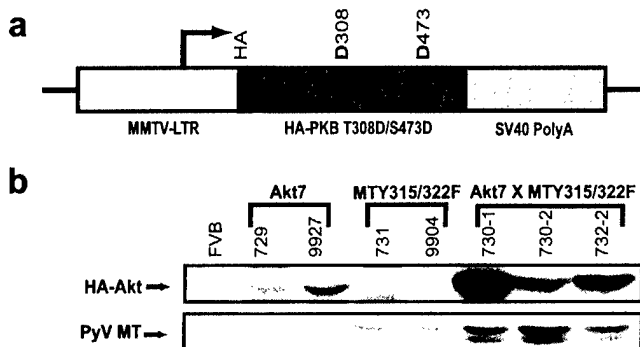


FIG. 1. Activated Akt transgene expression. (a) Structure of the MMTV/Akt transgene. The Bluescript vector backbone is represented by a thin line on either side of the expression cassette, with the white region corresponding to the MMTV-LTR derived from plasmid pAp, the black portion corresponding to the hemagglutinin tag, the dark grey region corresponding to the Akt (HAPKB308D/S473D) cDNA with aspartate substitutions at amino acid positions 308 and 473, and the mid-grey region corresponding to the transcriptional processing sequences derived from the SV40 early transcription unit. The transcription start site is indicated by an arrow. (b) Immunoblot analysis of expression of HAPKB and PyV mT in bitransgenic Akt7  $\times$  MTY315/322F strains. Note that Akt7  $\times$  MTY315/322F tumor samples coexpress both Akt and PyV mT proteins. The numbers above each lane indicate individual mouse identification numbers.

lated with the phosphorylation of FKHR, a member of the forkhead class of transcription factors, and induction of cyclin D1. Together these observations suggest that activation of Akt provides complementary cell survival signals that are required for mammary tumorigenesis.

#### MATERIALS AND METHODS

**Generation and identification of transgenics.** The cDNA encoding HAPKB308D473D was subcloned into pMMTV-SV40Pa (p206) (18). This construct was prepared and injected as previously described (35). Transgenic progeny were identified by Southern analysis using the *EcoRI-BamHI* (3900 to 4775) fragment of p206 (18) as a probe. Akt-MTY315/322F bitransgenics were generated by crossing MMTV/MTY315/322F males to MMTV/Akt7 females and were subsequently identified by identical Southern analysis.

**Histology and apoptosis assays.** Lower left mammary fat pad tissues were fixed in 4% paraformaldehyde, blocked in paraffin, sectioned at 5  $\mu$ m, stained with hematoxylin and eosin, and examined. Whole-mount preparations were pre-

TABLE 2. MMTV/Akt transgene expression in MMTV/Akt7 tissues<sup>a</sup>

Sex	Tissue	Expression <sup>b</sup> in strain:	
		Akt7	Akt10
Female	Mammary gland	++	+
	Brain	—	—
	Heart	—	—
	Kidney	—	—
	Liver	—	—
	Lung	—	—
	Ovary	—	—
	Salivary	—	—
	Spleen	—	—
	Thymus	—	—
	Epididymis	++++	++++
Male	Seminal vesicles	++	++++
	Testes	—	—

<sup>a</sup> Expression of the Akt transgene was determined by Western blot analysis using the HA-11 monoclonal antibody (Babco) on 250  $\mu$ g of total protein lysate precleared in protein G-Sepharose.

<sup>b</sup> Relative levels of transgene expression: —, not detected; +, low; ++, intermediate; +++, high; +++++, very high.

pared from the lower right mammary fat pad as previously described (35). In situ apoptosis assays were performed with the Apoptag Peroxidase In Situ Apoptosis Detection Kit (Intergen) as described previously (35).

**RNA isolation and analysis.** RNA was isolated from mammary glands and analyzed by RNase protection using simian virus 40 (SV40) polyadenylation-specific (SPA) and PGK-1 ribonucleotide protection probes as previously described (35).

**Protein extraction and analysis.** Tissue from various organs was flash frozen in liquid nitrogen and stored at  $-80^{\circ}\text{C}$  or immediately lysed. Protein lysates were prepared as previously described (35). All immunoblots and immunoprecipitations were carried out as previously described (35) with the following exceptions. Antihemagglutinin (anti-HA) immunoblot analyses of mammary tissue from the FVB/n, Akt7, MTY315/322F, and Akt7  $\times$  MTY315/322F strains were performed on 250  $\mu$ g of total protein lysate. Lysates were precleared in protein G-Sepharose and subjected to anti-HA immunoblot analysis with HA-11 monoclonal antibody (Babco) (1:1,000). PyV mT was immunoprecipitated from 2 mg of total protein lysate with 2  $\mu$ g of mouse monoclonal Pab762 (courtesy of S. Dilworth) and subjected to anti-mT immunoblot analysis with rat monoclonal Pab701 (1:1,000). Anticytokeratin immunoblot analysis was carried out on 250  $\mu$ g of total protein lysate using Troma-1 rat monoclonal antibody from ascites (1:50). Cyclin D1 analysis was carried out on 50  $\mu$ g of total protein using the anti-cyclin D1 72-13G monoclonal antibody from Santa Cruz. FKHR analysis was carried out on 50  $\mu$ g of total protein using the anti-FKHR N-18 polyclonal antibody from Santa Cruz and the anti-phospho-FKHR (Ser256) antibody from New England Biolabs.

Akt immunoblotting was carried out on total lysate using the anti-Akt antibody from New England Biolabs. Akt kinase activity assays were carried out on immunoprecipitates from total lysate using the anti-PH domain PKB antibody from UBI and the cross-tide peptide as substrate. Glycogen synthase kinase 3 (GSK-3) analysis was carried out on total lysate using anti-GSK-3 antibodies from New England Biolabs.

#### RESULTS AND DISCUSSION

To further assess the importance of the PI3K/Akt signaling pathway in PyV mT-induced tumorigenesis and metastasis, we derived transgenic mice that express a constitutively active version of Akt (HAPKB308D473D or Akt-DD), which mimics the active phosphorylated state of the protein (1), in the mammary gland (Fig. 1a). To distinguish between the transgene-derived and endogenous Akt protein, an HA epitope tag was placed in frame at the amino terminus of the activated Akt protein (Fig. 1a). Initially, 11 activated MMTV/Akt founder lines were derived. Nine of these lines passed the transgene to their offspring, and a screen for expression of the activated Akt

TABLE 1. MMTV/Akt transgene expression in mammary gland<sup>a</sup>

Line	Expression <sup>b</sup>
Akt1	—
Akt2	—
Akt3	—
Akt4	—
Akt5 <sup>c</sup>	ND
Akt6	—
Akt7	++
Akt8	—
Akt9	+
Akt10	+
Akt11 <sup>c</sup>	ND

<sup>a</sup> Expression of the Akt transgene in the mammary gland was determined via RNase protection analysis on 20  $\mu$ g of total RNA with a probe directed against the SV40 poly(A) region of the transgene.

<sup>b</sup> Relative levels of transgene expression: ND, no data; —, not detected; +, low; ++, high.

<sup>c</sup> Strain did not pass transgene.

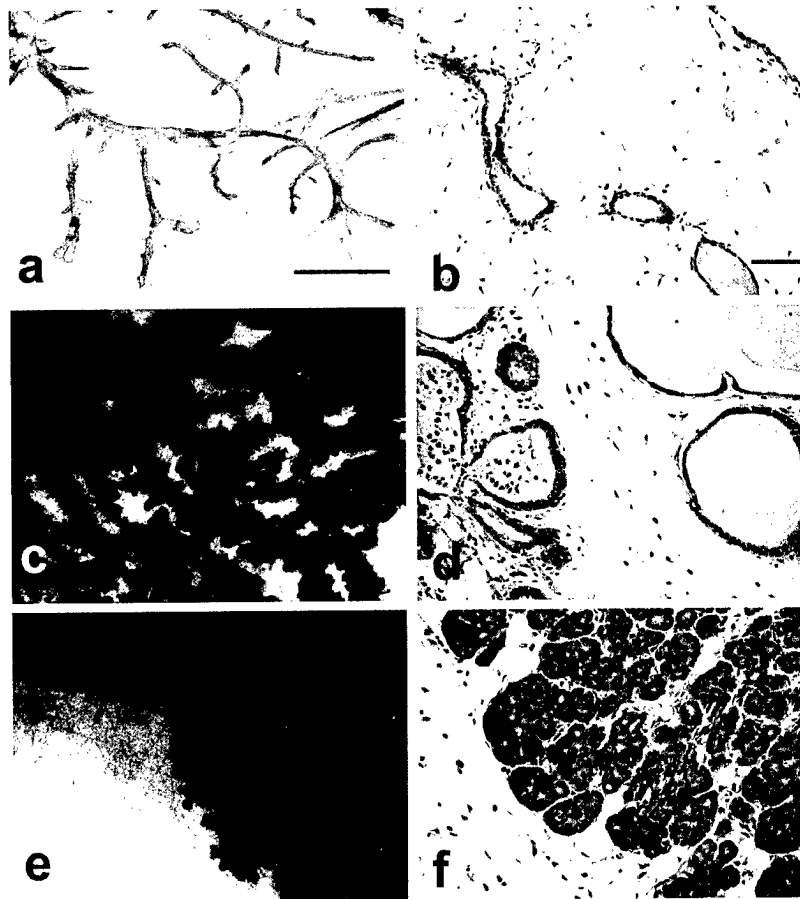


FIG. 2. Coexpression of Akt and mutant PyV mT oncogene results in the induction of multifocal mammary tumors. These digital images illustrate the histological patterns observed in the Akt7 (a and b), MTY315/322F (c and d), and Akt7  $\times$  MTY315/322F (e and f) bigenic mice. Note that the whole-mount preparations (a, c, and e) demonstrate that the Akt strains have a relatively normal mammary tree (a) compared to the cystic hyperplasias seen in the MTY315/322F strains at the same age (c) (8 weeks) (scale bar = 1 mm). In contrast, the bigenic mammary gland does not fill the fat pad (e) and is a solid mass at this age (f). The histological patterns seen at high magnification (scale bar = 0.01 mm) demonstrate that the Akt7 strain has a normal epithelium (b), while the MTY315/322F strain has a cystic hyperplasia of the ducts and glands without significant atypia (d). In contrast, the Akt7  $\times$  MTY315/322F cross has acinar or lobular hyperplasia with low-grade atypia at 8 weeks (f). Normal mammary gland morphologies for the FVB strain can be viewed at the following website: <http://ccm.ucdavis.edu/tgmouse/wmtable.htm>.

transgene revealed expression in the mammary gland in three of these lines (Table 1). The tissue specificity of transgene protein product expression of two of these lines (MMTV/Akt7 and MMTV/Akt10) was determined, and the higher expresser (MMTV/Akt7) was chosen for further study (Table 2). To confirm that activated Akt protein product was expressed in the mammary epithelium of transgenic mice, multiple mammary tissue extracts from the Akt7 line were subjected to anti-HA immunoblot analysis. The results revealed that virgin mammary glands from these strains were expressing significant levels of the transgene-derived Akt protein (Fig. 1b).

To ascertain whether elevated expression of activated Akt could interfere with normal mammary gland development, whole-mount analyses of both virgin and involuting mammary glands were conducted. Virgin female glands from MMTV/Akt strains were histologically and morphologically identical to FVB/n female controls (Fig. 2a and b). Consistent with these observations, female virgin Akt transgenic mice have yet to develop mammary tumors after a year of observation. This observation is further supported by the observation that multiparous Akt transgenic females, which would have undergone

multiple periods of high transgene expression, have also failed to exhibit tumors. Given the importance of apoptotic cell death in mammary gland involution, we next examined whether mammary gland involution was adversely affected in the activated Akt strain. To explore this possibility, mammary glands from the wild-type and activated Akt strains were examined at 1, 3, and 7 days postparturition. In contrast to wild-type control animals, which exhibited extensive involution at 1 and 3 days postparturition (Fig. 3a, c, e, and g), the Akt7 animals displayed a dramatic defect in mammary gland involution (Fig. 3b, d, f, and h). However, the Akt7 mammary glands eventually underwent full involution at 7 days postparturition (data not shown), likely due to a drop in the hormonally responsive MMTV-driven transgene expression in the activated Akt strain.

To assess whether the observed delay in mammary gland involution was due to a defect in the induction of apoptotic cell death, terminal deoxynucleotidyltransferase-mediated dUTP-biotin nick end labeling (TUNEL) analyses were conducted on involuting mammary epithelium derived from FVB/n and Akt7 strains (Fig. 4). The results revealed that mammary glands

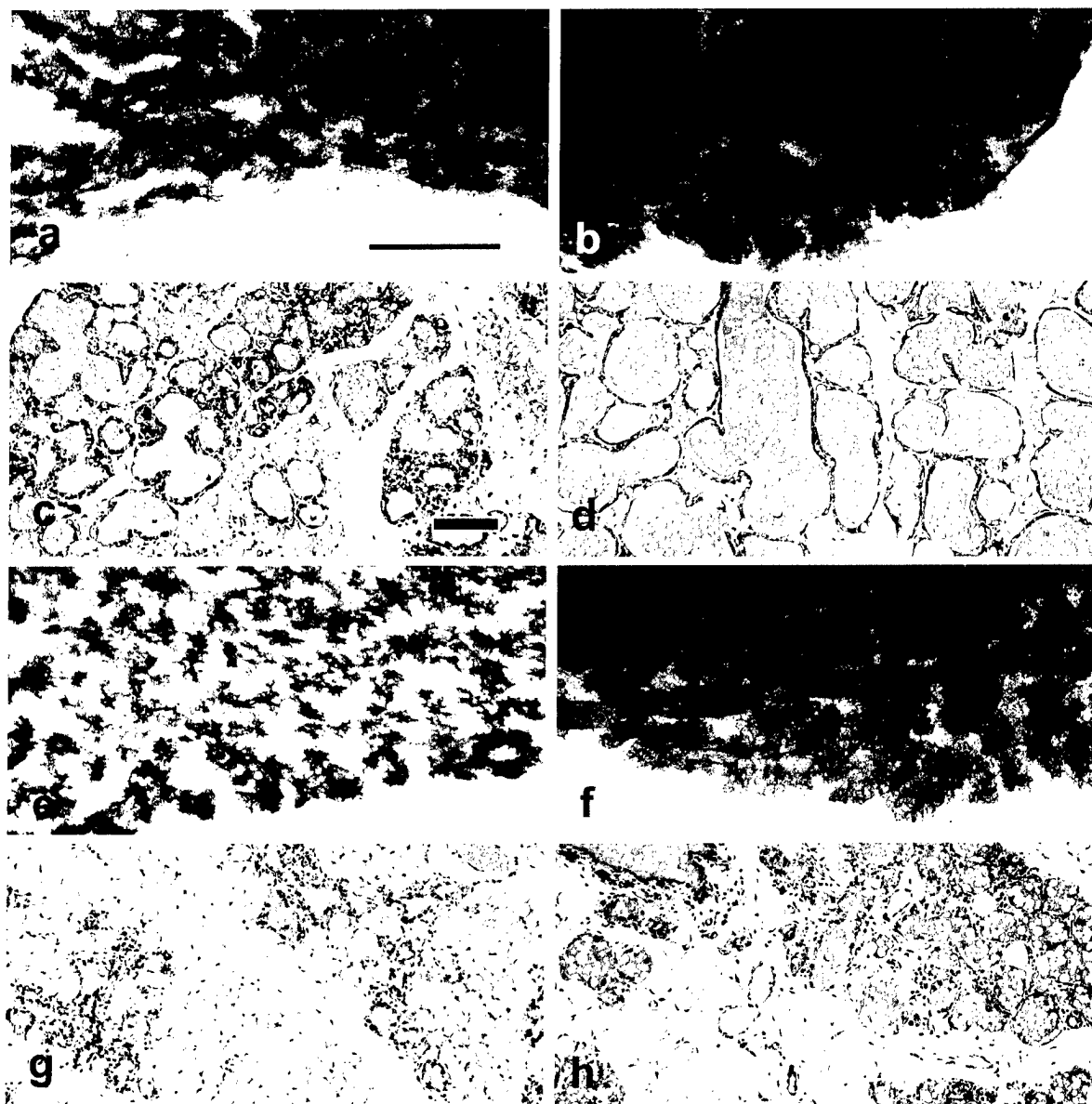


FIG. 3. Mammary epithelial expression of Akt results in defect in mammary gland involution. Digital images of the involution patterns in wild-type (a, c, e, and g) and Akt7 (b, d, f, and h) mammary glands. The images compare whole-mount preparations (a, e, b, and f) of the mammary gland (scale bar = 1 mm) with the histological pattern (c, d, g, and h) (scale bar = 0.1 mm) on days 1 (a to d) and 3 (e to h) of involution. Note the delayed involution in the Akt7 mouse mammary gland (b to h).

derived from the involuting FVB/n glands exhibited elevated levels of apoptotic cell death relative to mammary epithelium of the Akt7 strain (compare Fig. 4a and b). Taken together, these observations argue that activation of Akt can interfere with normal mammary gland involution by attenuating apoptotic death in the involuting mammary gland.

Although these data suggest that the Akt-DD mutant can interfere with apoptotic cell death during mammary gland involution, its role in mammary tumorigenesis is unclear. To explore whether active Akt expression could complement the defect in tumorigenesis exhibited by transgenic mice expressing the mutant PyV mT decoupled from the PI3K/Akt signaling pathway, bitransgenics expressing both the Akt transgene and the mutant mT transgene (MTY315/322F) were derived

(Fig. 1b) and monitored for tumor formation by physical palpation. The results of these analyses revealed that bitransgenic mice developed multifocal mammary tumors with 100% penetrance with an average latency of 46 days (Fig. 5a). In contrast, physical palpation of two independent cohorts of female mice carrying the mutant PyV mT transgene alone revealed a significant delay in the onset of tumor formation with average latencies of 123 and 119 days, respectively (Fig. 5a). In addition, these tumors were focal in nature, arising next to hyperplastic mammary epithelium. Consistent with these kinetic analyses, whole-mount analyses of virgin mammary glands of bitransgenic mice revealed a dramatic difference in the extent of tumor growth (compare Fig. 2e and f to c and d). In contrast to the diffuse cystic hyperplasias exhibited by the mutant PyV

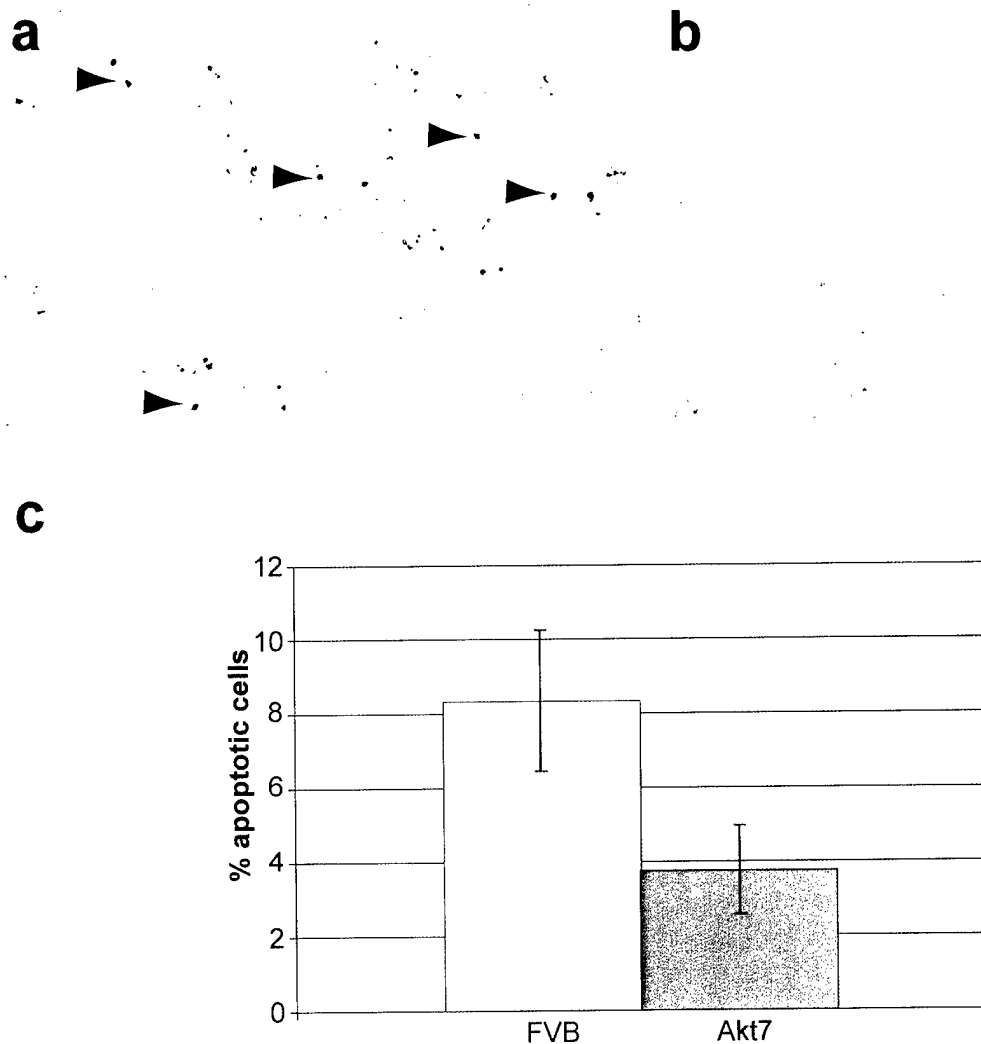


FIG. 4. Mammary epithelial expression of Akt results in decreased mammary gland apoptosis during involution. (a and b) TUNEL analysis of involuting mammary glands from FVB/n (a) and Akt7 (b) at 3 days postparturition. Arrows indicate representative apoptotic cells. (c) Mammary apoptotic indices of FVB/n and Akt7 at 3 days postparturition. Values shown represent the percentage of total cells stained positive for apoptosis by TUNEL assay in age-matched singly parous female mice at 15 weeks of age.

mT strains, female transgenic mice coexpressing the mutant PyV mT and activated Akt transgenes exhibited polyclonal differentiated carcinomas. In agreement with these analyses, these lesions could be subcutaneously transplanted into syngeneic recipients. To confirm that bitransgenics expressing MTY315/322F and activated Akt exhibited elevated Akt kinase activity, we examined the total Akt kinase activity against a peptide substrate in virgin FVB/n, MTY315/322F, and bitransgenic mammary glands. These studies revealed an approximately fivefold increase in the total Akt kinase activity in the bitransgenic mammary glands as compared to those of MTY315/322F transgenics (Fig. 6a). The minimal increases in endogenous Akt phosphorylation (Fig. 6b) would suggest that the majority of the Akt kinase activity is derived from the activated mutant. However, these results do not completely preclude a mechanism whereby endogenous Akt is in some way activated via the combination of Akt-DD and MTY315/322F and contributes to tumor formation.

As the mammary epithelial hyperplasias associated with the mutant PyV mT strains exhibit elevated levels of apoptotic cell death, we measured the degree of apoptotic cell death in mammary glands derived from the mutant PyV mT or bitransgenic mice. The results revealed that mammary epithelial expression of activated Akt resulted in a dramatic repression of the high rates of apoptotic cell death in PyV mT mutant tissue decoupled from the PI3K (Fig. 5b). Taken together, these observations argue that the dramatic acceleration of mammary tumorigenesis exhibited by these strains is due to the ability of activated Akt to suppress the elevated apoptotic cell death displayed by mutant PyV mT mammary epithelium.

Although the active, transgenic Akt is able to complement the mutant PyV mT strains for the induction of mammary tumors, only 20% of the tumor-bearing mice have developed lung metastases more than 8 weeks after the initial palpation of the mammary tumor ( $n = 10$ ) at tumor loads comparable to those observed in mice expressing wild-type mT at similar time

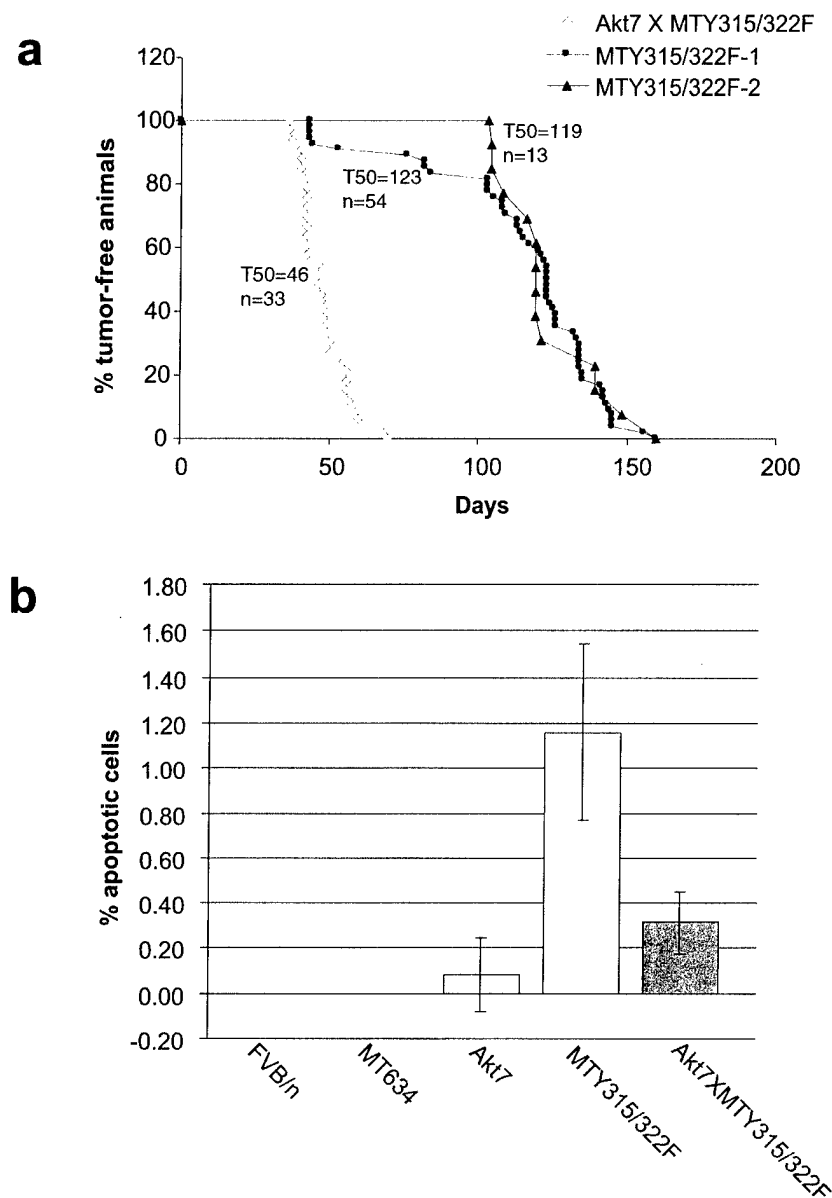


FIG. 5. Mammary tumor kinetics and apoptotic indices in transgenic strains. (a) Mammary tumor kinetics of MTY315/322F and Akt7  $\times$  MTY315/322F strains. Two different kinetics curves are shown for the MTY315/322F strain, from the original published data (MTY315/322F-1) and confirmatory data us (MTY315/322F-2), to account for possible differences in palpation technique between researchers. The age indicated is that at which a mammary tumor is first palpable in each transgenic strain. The number of animals analyzed for each strain ( $n$ ) and the median age at which tumors were palpable are also shown. (b) Mammary apoptotic indices of FVB/n, MT634 (wild-type mT), Akt7, MTY315/322F, and Akt7  $\times$  MTY315/322F strains. Values shown represent the percentage of total cells stained positive for apoptosis by TUNEL assay in virgin female mice at 10 to 12 weeks of age.

points. The penetrance of the metastatic phenotype is comparable to the 30% metastasis levels exhibited by the parental mutant PyV strains. In contrast, 100% of mice expressing wild-type mT show multiple lung metastases at comparable time points and tumor loads (18). These observations argue that while expression of active Akt can complement the defect in mammary tumor progression, it is unable to rescue the defect in metastatic progression.

To further explore the molecular basis for the observed cooperative interaction between activated Akt and the mutant PyV mT oncogene, we assessed the status of some of the known

targets of Akt, including BAD (9), I- $\kappa$ -B (20), and the FKHR forkhead transcription factor (34).

No significant differences in either BAD-Ser136 phosphorylation or I- $\kappa$ -B levels were observed between the various transgenic strains (data not shown). Caspase 9, another Akt substrate (4), was not examined, as the Akt phosphorylation site found in human caspase 9 is absent in mouse caspase 9 (17). However, analysis of protein lysates from mammary tissues of 8-week-old virgin FVB/n, Akt7, mutant PyV mT, and bigenic mice subjected to immunoblot analyses with phospho-specific antisera to serine 256 of FKHR (Fig. 7a) revealed that

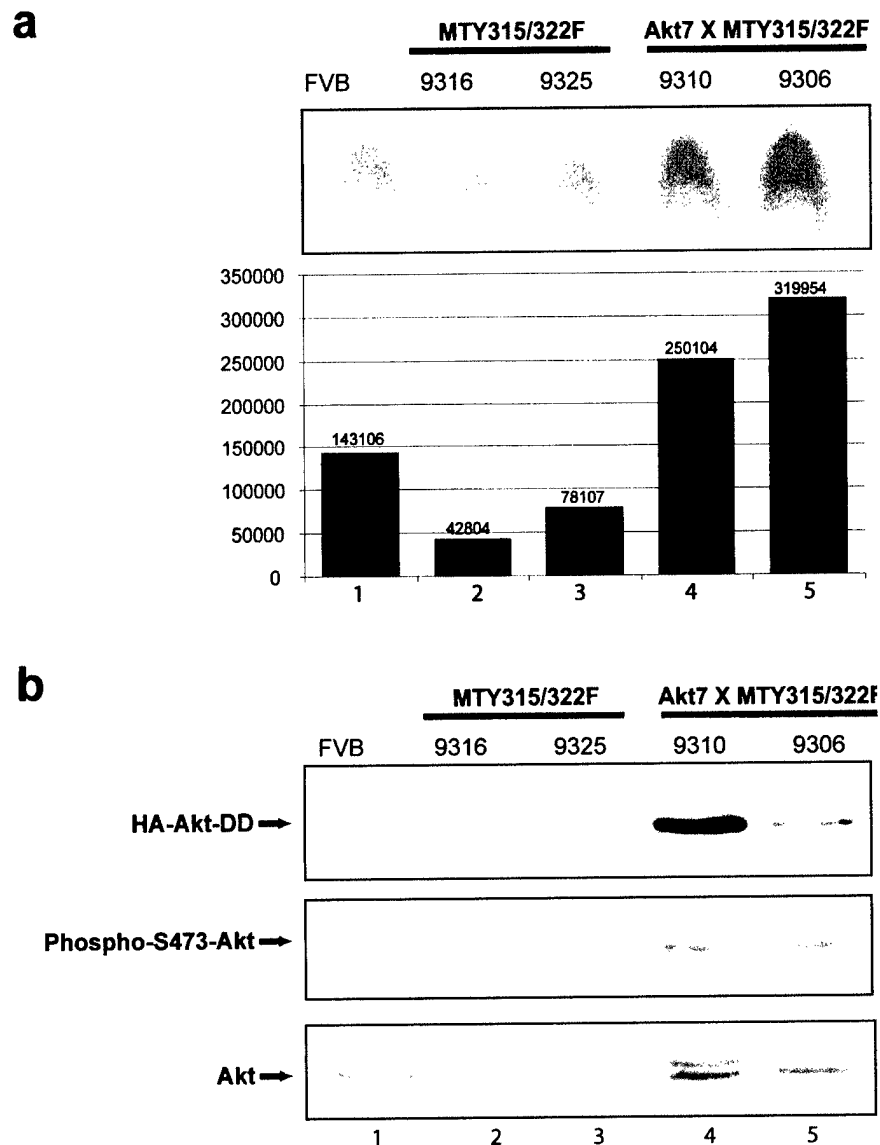


FIG. 6. Akt kinase activity in transgenic strains. (a) Total Akt kinase activity analysis in 8- to 10-week-old virgin females from FVB/n (lane 1), MTY135/322F (lanes 2 and 3), and bitransgenic Akt7  $\times$  MTY315/322F (lanes 4 and 5) strains. Assays were conducted using the cross-tide peptide as an Akt kinase substrate. Kinase activities were quantified by phosphorimager analysis and are represented here both graphically and numerically. (b) Immunoblot analysis of expression of HA-Akt-DD, phospho-S473-Akt, and Akt in 8- to 10-week-old virgin females from FVB/n (lane 1), MTY135/322F (lanes 2 and 3), and bitransgenic Akt7  $\times$  MTY315/322F (lanes 4 and 5) strains. All tissues were derived from 8- to 10-week-old virgin mammary glands. The arrows indicate the migration of transgenic HA-Akt-DD (upper panel), phospho-S473-Akt (middle panel), and total Akt (bottom panel). The numbers above each lane indicate individual mouse identification numbers.

the mammary tissue samples derived from the bitransgenic animals expressed elevated levels of phosphorylated FKHR protein relative to the other tissue samples (second panel). The differences in the phosphorylation status of FKHR proteins were not due to levels of FKHR protein, since most of the tissues expressed comparable levels of FKHR protein (upper panel). In addition, the differences in the phosphorylation status could not be due to variation in epithelial content, since these samples expressed comparable levels of cytokeratin 8 (lower panel). Consistent with these observations, we have demonstrated an identical pattern of FKHR phosphorylation in a second independent cohort of samples (data not shown). To further explore this observation we examined the status of

p27 (Kip1), as forkhead transcription factors have been shown to target expression of the cell cycle regulator p27 (13, 23, 24). In particular, adenoviral expression of a constitutively active version of FKHR in the human renal cancer cell line 786-O cells induces expression of p27 (24). However examination of p27 levels by Western blotting revealed no apparent decreases in p27 levels in the bitransgenic animals as compared to MTY315/322F and FVB/n controls (Fig. 7b, lower panel). This apparent discrepancy may be due to the different nature of the tissues and signals involved in these experiments.

Nevertheless, another potential target for the PI3K/Akt kinase axis is the cell cycle machinery. Indeed, it has previously been demonstrated that suppression of the PI3K signaling



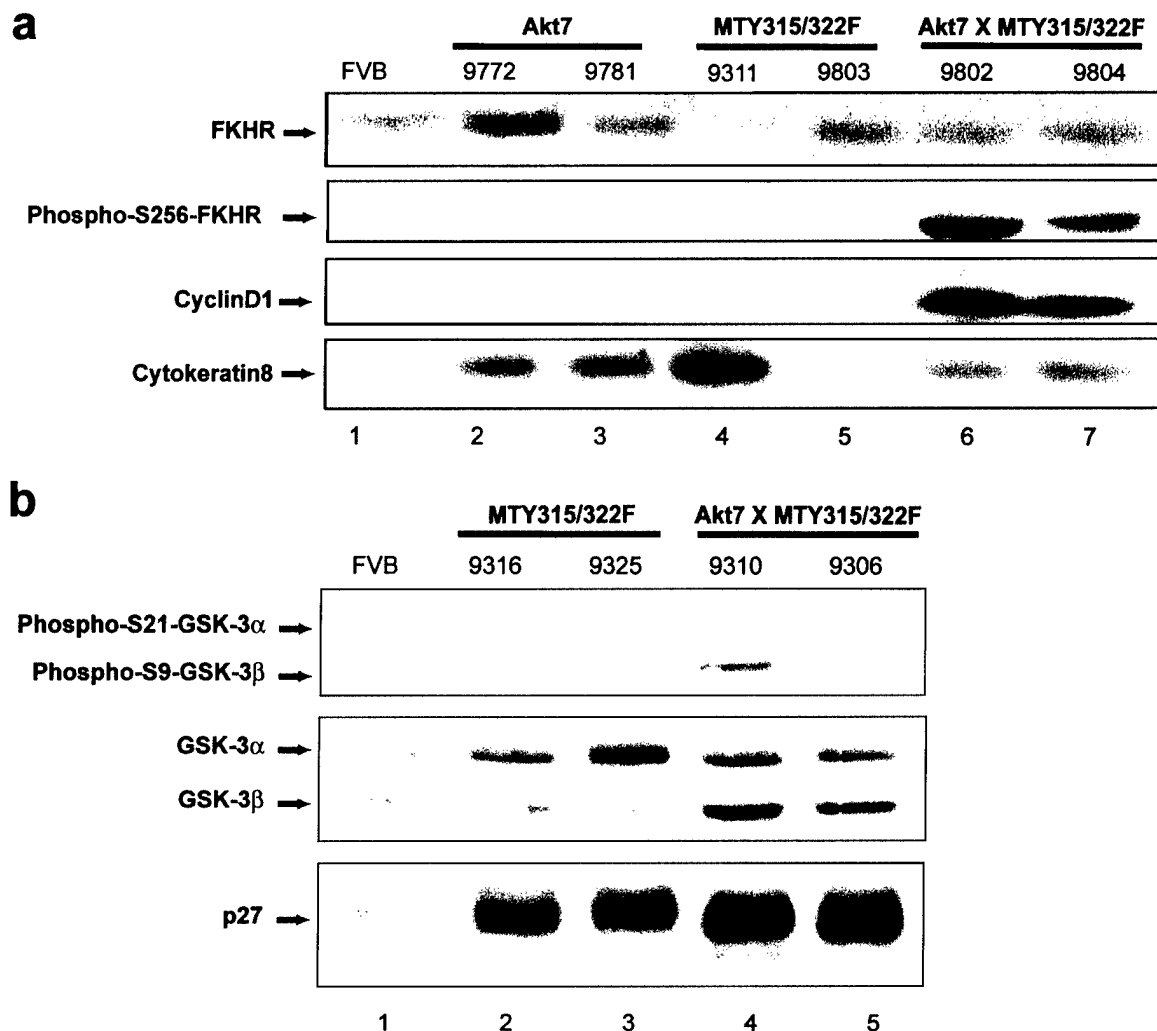


FIG. 7. Coexpression of activated Akt and MTY315/322F results in FKHR phosphorylation at serine 256 and increased cyclin D1 levels but does not affect GSK-3 phosphorylation or p27 levels. (a) Immunoblot analysis of expression of FKHR, phospho-FKHR (Ser256), cyclin D1, and cyokeratin in 8- to 10-week-old virgin females from FVB/n (lane 1), Akt7 (lanes 2 and 3), MTY135/322F (lanes 4 and 5), and bitransgenic Akt7 × MTY315/322F (lanes 6 and 7) strains. All tissues were derived from 8- to 10-week virgin mammary glands. The arrows indicate the migration of FKHR (upper panel), phospho-FKHR (Ser256) (second panel), cyclin D1 (third panel), and cyokeratin proteins (lower panel). The numbers above each lane indicate individual mouse identification numbers. (b) Immunoblot analysis of expression of phospho-S21-GSK-3α, phospho-S9-GSK-3β, GSK-3α/β, and p27 in 8- to 10-week-old virgin females from FVB/n (lane 1), MTY135/322F (lanes 2 and 3), and bitransgenic Akt7 × MTY315/322F (lanes 4 and 5) strains. All tissues were derived from 8- to 10-week virgin mammary glands. The arrows indicate the migration of phospho-S21-GSK-3α and phospho-S9-GSK-3β (upper panel), GSK-3α/β (middle panel), and p27 (lower panel). The numbers above each lane indicate individual mouse identification numbers.

pathway by expression of the PTEN tumor suppressor results in downregulation of cyclin D1 expression and cell cycle arrest (32, 36). To determine whether the levels of cyclin D1 could be influenced by Akt activation, the identical set of mammary tissues were subjected to immunoblot analyses with cyclin D1-specific antibodies. The results of these analyses revealed that the bitransgenic tissues coexpressing both Akt-DD and the mutant PyV mT oncogene exhibited dramatically elevated levels of cyclin D1 (Fig. 7a, third panel). The differences in cyclin D1 protein were not due to increased levels of cyclin D1 transcripts, since these samples expressed comparable levels of cyclin D1 transcript (data not shown). Taken together these observations suggest that activation of FKHR and cyclin D1

proteins are involved in promoting tumor progression in these strains.

The studies outlined above provide compelling evidence that expression of activated Akt is involved in promoting tumor progression by providing a critical cell survival pathway. Consistent with this contention, mammary epithelial expression of Akt can result in profound delays in mammary gland involution, a process involving extensive apoptotic cell death. Moreover, coexpression of activated Akt can suppress the elevated rates of apoptotic cell death that are observed in mammary epithelial hyperplasias induced by the mutant PyV mT decoupled from the PI3K signaling pathway. However, because mammary epithelial expression of activated Akt does not result

in the induction of mammary tumors itself, tumorigenesis requires the constitutive activation of other signaling pathways that are recruited by the mutant PyV mT oncogene, including the Src family kinases and Shc/Grb2/Ras pathway. Consistent with this view, we have observed that efficient phosphorylation of the FKHR protein requires the concerted activation of both Akt and the mutant PyV mT oncogene (Fig. 7). A similar requirement for coactivation of Akt and mutant PyV mT was also noted for the induction of cyclin D1. In this regard, it has recently been reported that the cooperation of Ras and Akt are required for the efficient transformation of primary glial cells (19). A potential mechanism for the increased levels of cyclin D1 was suggested by the ability of Akt and mitogen-activated protein kinases to phosphorylate and inhibit GSK-3 (8, 33), which has been shown to target cyclin D1 for proteasomal degradation (12). However, analysis of GSK-3 phosphorylation showed no significant increases in the bitransgenic strain as compared to FVB/n and MTY315/322F controls, once differences in GSK-3 levels were accounted for (Fig. 7b, upper and middle panels). Even so, these results suggest that the concerted activation of both cell survival and proliferative signaling pathways may be a common requirement for oncogenic transformation of primary cells.

Although our studies suggest that activated Akt can cooperate with these signaling pathways to efficiently induce mammary tumorigenesis, the observed low rates of metastasis suggest the involvement of other Akt-independent signals downstream of middle T in the potent metastatic phenotype exhibited by wild-type PyV mT. While these signals are in all likelihood PI3K dependent, we cannot exclude the possibility that signaling molecules other than PI3K may bind to and be activated via the 315 and 322 phosphorylated tyrosine residues. However, PI3K activation does modulate the activity of members of the Rho family of GTP-binding proteins (21, 25, 27, 29) and the integrin-linked kinase (11). This modulation is highly relevant, as the roles of these sets of signaling molecules in cell migration and adhesion implicates them in metastatic progression (10, 28). Further exploration of these PI3K-dependent pathways will provide important insight into the molecular basis of the metastatic phenotype.

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## Transgenic mouse models of human breast cancer

John N Hutchinson<sup>1,2</sup> and William J Muller<sup>\*1,2,3,4</sup>

<sup>1</sup>Institute for Molecular Biology and Biotechnology, McMaster University, 1280 Main St. W., Hamilton, Ontario, Canada, L8S 4K1; <sup>2</sup>Department of Biology, McMaster University, 1280 Main St. W., Hamilton, Ontario, Canada, L8S 4K1; <sup>3</sup>Department of Biochemistry, McMaster University, 1280 Main St. W., Hamilton, Ontario, Canada, L8S 4K1; <sup>4</sup>Department of Pathology and Molecular Medicine, McMaster University, 1280 Main St. W., Hamilton, Ontario, Canada, L8S 4K1

The pathogenesis of human breast cancer is thought to involve multiple genetic events, the majority of which fall into two categories, gain of function mutations in proto-oncogenes such as *c-myc*, cyclin D1, ErbB-2 and various growth factors which are involved in supporting cell growth, division and survival, and loss of function mutations in so called 'tumor suppressor' genes, such as *p53*, which are involved in preventing unrestrained cellular growth. A number of mouse systems exist to address the significance of these mutations in the pathogenesis of breast cancer including transgenic mice expressing high levels of a specific gene in target tissues and knockout mice in which specific genes have been ablated via homologous recombination. More recently, the combination of these techniques to create bigenics as well as the use of 'knockin' and conditional tissue specific gene targeting strategies have allowed the models more reflective of the human disease to be devised. Studies with these models have not only implicated particular genetic events in the progression of the disease but have emphasized the complex, multi-step nature of breast cancer progression. These models also provide the opportunity to study various aspects of the pathogenesis of this disease, from hormonal effects to responses to chemotherapeutic drugs. It is hoped that through the combined use of these models, and the further development of more relevant models, that a deeper understanding of this disease and the generation of new therapeutic agents will result. *Oncogene* (2000) 19, 6130–6137.

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### Introduction

The pathogenesis of breast cancer is thought to involve multiple genetic events. Karyotypic and epidemiological analyses of mammary tumors at various stages suggest that breast carcinomas become increasingly aggressive through the stepwise accumulation of genetic changes (Dupont and Page, 1985). The majority of genetic changes found in human breast cancer fall into two categories, gain of function mutations in proto-oncogenes, which are involved in supporting cell growth, division and survival, and loss of function mutations in so called 'tumor suppressor' genes, which are involved in preventing unrestrained cellular growth. The majority of gain of function

mutations in human primary breast cancers involve amplifications in one of three chromosomal regions, the *c-myc* and *erbB-2* proto-oncogenes or the chromosomal band 11q13 (Lidereau *et al.*, 1988). Loss of function mutations in primary human breast cancers include changes in the known tumor suppressor *p53* as well as in the familial cancer markers of the BRCA gene family. Additionally, multiple regions of loss of heterozygosity (LOH) are observed in primary human breast cancers (Bieche and Lidereau, 1995; Callahan *et al.*, 1992; Garcia *et al.*, 1999). It is thought that these regions of LOH affect as yet unidentified putative tumor suppressors. Indeed allelic loss of the PTEN region has been noted in a subset of aggressive breast cancers (Garcia *et al.*, 1999).

A number of mouse systems exist to address the significance of these mutations in the pathogenesis of breast cancer. On the most basic level, the use of transgenic mice expressing high levels of a specific gene in a target tissue allows the involvement of a given gene in the pathogenesis of breast cancer to be addressed. Alternatively, the ablation of specific genes via homologous recombination also allows researchers to determine the role of a gene in breast cancer progression. More recently, the combination of these techniques to create bigenics as well as the use of 'knock-in' and conditional tissue specific gene targeting strategies have allowed the creation of models more reflective of the human disease to be devised.

### Transgenic mouse models of gain of function mutations

A number of transgenic promoters have been employed to target transgene expression to the mammary gland. A majority of the transgenics generated have employed either the mouse mammary tumor virus long terminal repeat (MMTV) or the whey acidic protein promoter (WAP). The MMTV-LTR is active throughout mammary development and its transcriptional activity increases during pregnancy (Pattengale *et al.*, 1989). In contrast, the WAP promoter is only active in the mid-pregnant mammary gland. Thus, it is apparent that the phenotypes exhibited by WAP and MMTV transgenics may depend upon the developmental stage of the individual mouse examined. Other less common promoters employed include the 5' flanking region of the C3(1) component of the rat prostate steroid binding protein, beta-lactalbumin, metallothionein and tetracycline responsive promoters.

\*Correspondence: WJ Muller

## Models for genetic regions amplified in human breast cancer

### *c-myc*

The *c-myc* gene encodes for a transcription factor that is frequently amplified in human tumors (Berns *et al.*, 1992; Bieche and Lidereau, 1995; Escot *et al.*, 1986). Multiple transgenic studies in which the *myc* gene was overexpressed under the control of mammary specific promoters have indicated an important role for *myc* in the progression of breast cancer (Leder *et al.*, 1986; Schoenenberger *et al.*, 1988; Stewart *et al.*, 1984). The first of these studies used the MMTV promoter to over-express *myc* in the mammary glands of mice and resulted in spontaneous mammary adenocarcinomas in two distinct lines by 4 to 8 months of age (Stewart *et al.*, 1984). A second transgenic study also using the MMTV promoter to overexpress *myc* resulted in the formation of locally invasive mammary tumors in four multiparous females by 10 to 19 months of age (Leder *et al.*, 1986). Interestingly, in one of MMTV/*myc* transgenic strains, *c-myc* expression was detected in a wide range of tissues. Despite the broad pattern of tissue specific expression, these mice developed a limited subset of tumor types including mammary tumors. Thus elevated expression of *c-myc* appears capable of inducing tumors in selected tissue sites.

Elevated expression of *myc* in the mammary gland has also been achieved by placing the *c-myc* oncogene under the transcriptional control of the WAP promoter (Schoenenberger *et al.*, 1988). In these transgenic strains, 80% of female transgenics develop multiple tumors affecting single or multiple glands after two pregnancies at ages as early as 2 months (Schoenenberger *et al.*, 1988). Together they demonstrate that *c-myc* can induce mammary tumor formation when overexpressed in the mammary gland. However, the fact that overexpression of *c-myc* does not result in transformation of the entire mammary gland, as normal mammary epithelium is also present in these strains, reveals that additional genetic events are required for the development of overt mammary carcinomas. In this sense, these models accurately reflect the nature of the progression of human breast cancer.

### *Cyclin D1*

Cyclins regulate the activation of cyclin-dependent kinases (CDK's) allowing cell cycle progression, S phase entry and DNA replication. A variety of lines of evidence have linked cyclins to the progression of breast cancer. Foremost, the *cyclin D1* gene is found within the 11q13 region, which is amplified in 15–20% of primary human breast cancers (Bieche and Lidereau, 1995; Brison, 1993). Overexpression of *cyclin D1* under control of the MMTV promoter results in proliferative abnormalities in the mammary gland, with significant lobulo-alveolar development shortly after sexual maturity is reached. Significantly, eight of 12 mice from three distinct transgenic lines developed focal mammary tumors with a mean onset of 18 months (Wang *et al.*, 1994). As with the *c-myc* transgenic models, the long latency and focal nature of these tumors suggests that although *cyclin D1* can

promote mammary tumorigenesis, additional genetic changes are needed for the development of overt mammary carcinomas. Consistent with this view, mammary epithelial expression of *cyclin D1* has been implicated as an important event in mammary tumor induced by activated Src kinases, integrin linked kinase (ILK) and ErbB-2 (Lee *et al.*, 1999, 2000; Radeva *et al.*, 1997). Conversely germline inactivation of *cyclin D1* results in impaired mammary epithelial gland development (Fantl *et al.*, 1999). Collectively these observations suggest that *cyclin D1* plays a critical role in both normal mammary gland development and mammary tumorigenesis.

### *ErbB-2*

ErbB-2 is a member of the EGFR family of receptor tyrosine kinases (RTKs). This family is comprised of four closely related type I RTKs that include the EGFR, ErbB-2 (Neu, HER2), ErbB-3 (HER3), and ErbB-4 (HER4) (Hynes and Stern, 1994; Olayioye *et al.*, 2000). Signaling in these receptors involves the formation of homo and hetero-dimers in response to ligand stimulation. This dimerization results in the phosphorylation of specific tyrosine residues on the receptor. These phosphorylated tyrosines then offer docking sites for the SH2 and SH3 (PTB) domains of various endogenous signaling molecules that are able to interact with the receptor and transduce the signal (Dankort and Muller, 2000; Hynes and Stern, 1994). Originally, *erbB-2* was described as the oncogene *neu* found in chemically induced neuroblastomas in rats (Schechter *et al.*, 1984). Neu possesses a valine-glutamic acid substitution in its transmembrane domain that results in the constitutive aggregation and activation of the receptor in the absence of ligand (Bargmann *et al.*, 1986a,b; Dankort and Muller, 2000; Stern *et al.*, 1986; Xie *et al.*, 1995).

The importance of ErbB-2 in primary human breast cancer is highlighted by the fact that 20–30% of human breast cancers express elevated levels of ErbB-2 due to the genomic amplification of the *erbB-2* proto-oncogene (Slamon, 1987, 1989). Furthermore, its amplification and subsequent overexpression strongly correlates with a negative clinical prognosis in both lymph node positive (Hynes and Stern, 1994; Mansour *et al.*, 1994; Ravdin and Chamness, 1995) and node-negative (Andrulis *et al.*, 1998) breast cancer patients. Further evidence that overexpression of ErbB-2 results in an aggressive tumor type stems from studies showing that elevated ErbB-2 expression is observed in many *in situ* and invasive human ductal carcinomas but is rarely observed in benign breast disorders such as hyperplasias and dysplasias (Allred *et al.*, 1992; Mansour *et al.*, 1994). Significantly, ErbB-2 overexpression may be useful not only as a prognostic marker but as a predictive marker as well as HER-2 overexpression predicts tamoxifen resistance of the primary tumor (reviewed in Pegram *et al.*, 1998).

Multiple transgenic mouse studies have confirmed a direct role for ErbB-2 in mammary tumorigenesis each with their own level of relevance to the human disease. MMTV-driven overexpression of the oncogene *neu* or an analogous ERbB-2 transgene engineered to possess a similar activating mutation within the transmembrane domain results in the formation of mammary

adenocarcinomas that histologically resemble human comedocarcinomas (Muller *et al.*, 1988; Bouchard *et al.*, 1989; Cardiff and Muller, 1993; Guy *et al.*, 1996; Stocklin *et al.*, 1993).

Although these studies suggest a significant role for ErbB-2 in human breast cancer progression, the lack of a comparable mutation in human breast cancers suggests that the primary mechanism operating in human breast cancer is the overexpression of wild-type ErbB-2 and not its mutational activation (Lemoine *et al.*, 1990; Slamon, 1989; Zoll *et al.*, 1992). Consequently, a more relevant model in which a wild-type *neu* cDNA was expressed under MMTV control was generated to test the oncogenic potential of the wild-type receptor. These mice develop focal mammary tumors of similar comedocarcinoma-type morphology after an average of 7 months which frequently metastasize to the lung (Guy *et al.*, 1992). Further examination of the ErbB-2 status in these tumors revealed that tumors but not the adjacent normal mammary epithelium carried sporadic mutations in *neu* which resulted in its constitutive activation (Siegel *et al.*, 1994). These mutations were comprised of multiple in frame deletions, insertions or point mutations in the extracellular domain of *neu* and promoted the transforming ability of *neu* through the formation of intermolecular di-sulfide bonds (Siegel and Muller, 1996). To directly explore the importance of these activated forms of Neu, transgenic mice carrying altered Neu receptors were derived. Females from these lines develop multiple mammary tumors that frequently metastasize to the lung with a mean onset between that of the normal and point-activated alleles (Siegel *et al.*, 1999). Interestingly, tumor progression in these strains was associated with elevated levels of tyrosine-phosphorylated Neu and ErbB-3 (Siegel *et al.*, 1999). Consistent with these observations, a survey of primary human breast tumors revealed frequent co-expression of both ErbB-2 and ErbB-3 transcripts (Siegel *et al.*, 1999). These results suggest that ErbB-3 may be the critical heterodimerization partner for Neu in breast cancer progression.

Although the transmembrane point mutation has not been detected in primary human breast cancers overexpressing ErbB-2, studies have detected an alternative splice form in human breast cancers and breast cancer-derived cell lines (Kwong and Hung, 1998; Siegel *et al.*, 1999). Significantly, this splice isoform closely resembles the *neu* deletion mutants observed in the transgenic line overexpressing wildtype *neu* with a 16 amino acid deletion in the juxta-transmembrane region of ErbB-2. Like the sporadic *neu* mutants, this splice isoform is oncogenic due to its capacity to form constitutively active dimers. Conceivably the observed high rate of mutations observed in the transgene in the Neu transgenic strain reflects the fact that the transgene was originally derived from a *neu* cDNA that is incapable of undergoing alternative splicing. Further studies will be required to assess the significance of this splice isoform in the pathogenesis of human breast cancer. Taken together these transgenic studies strongly implicate the activation of ErbB-2 through receptor dimerization as a critical step in mammary tumorigenesis.

## Role of growth factors in breast cancer progression

### EGFR ligands

As alluded to above, the expression of EGFR family members plays a critical role in the induction of mammary cancers. Another way to activate members of the EGFR receptor family is through elevated expression of their ligands. Indeed, expression of EGFR ligands TGF- $\alpha$  and amphiregulin can be detected in erbB-2 induced mammary tumors (Kenney *et al.*, 1996). Transforming factor alpha is a peptide hormone first isolated from retrovirus-transformed cells and subsequently identified in the conditioned media of breast cancer-derived cell lines and in invasive ductal carcinomas. TGF- $\alpha$  possesses strong homology to EGF and like EGF acts as a ligand for the EGFR. TGF and EGFR expression has been found to coincide with normal mammary epithelial proliferation *in vivo* (reviewed in Humphreys and Hennighausen, 2000). Early studies with transgenic mice expressing TGF- $\alpha$  weakly in the mammary gland showed increased cellular proliferation and fat pad developmental defects (Sandgren *et al.*, 1990). These mice displayed mammary epithelial hyperplasias and dysplasias after multiple pregnancies (Sandgren *et al.*, 1990). Transgenic mice expressing TGF- $\alpha$  under MMTV control showed developmental defects and hyperplasias in virgin mice (Matsui *et al.*, 1990). These hyperplasias were observed to progress towards dysplasias with multiple pregnancies and increasing age, with 40% of multiparous animals showing tumors at 16 months of age (Halter *et al.*, 1992). More dramatic effects were achieved by targeting TGF- $\alpha$  to the mammary gland with the WAP promoter. Mice expressing TGF- $\alpha$  under WAP control showed increased incidence and shorter latency of tumor formation as compared to the MMTV models (Sandgren *et al.*, 1995). The relationship between mammary development and tumorigenesis is highlighted by the observation that these mice also displayed significant delays in mammary gland involution (Sandgren *et al.*, 1995). As these mice still required multiple pregnancies for tumors to form, it is possible that this delay in involution may act to provide an expanded population of proliferating epithelial cells predisposed to transformation (Humphreys and Hennighausen, 2000). However, the long latency observed once again indicates that additional genetic events are necessary for tumor progression in this model. In this regard, it is interesting to note that levels of Cyclin D1 were increased in tumors from the WAP-TGF- $\alpha$  mice (Sandgren *et al.*, 1995).

Another class of EGFR ligands that has been implicated in the induction of mammary cancers are members of the heregulin family (Chang *et al.*, 1997). Mammary specific expression of one of the neuregulin isoforms in transgenic mice initially resulted in generation of terminal end bud hyperplasias (Krane and Leder, 1996). However these transgenic mice eventually developed focal mammary tumors and co-expressed constitutively tyrosine phosphorylated ErbB-2 and ErbB-3 receptors. These observations reinforce the importance of ErbB-2 and ErbB-3 heterodimers in the induction of mammary cancers.

### Hepatocyte growth factor (HGF)

Another growth factor thought to play an important role in modulating the biological behavior of mammary epithelial cells is the hepatocyte growth factor. HGF and its receptor tyrosine kinase Met are involved in the development of the normal mammary gland (Niemann *et al.*, 1998; Yang *et al.*, 1995). Several studies have also shown overexpression of both Met and HGF in human breast cancers (Lamszus *et al.*, 1997; Tuck *et al.*, 1996; Yamashita *et al.*, 1994). Two studies have generated mice which express an activated form of the Met receptor under control of the metallothionein promoter with varying results (Jeffers *et al.*, 1998; Liang *et al.*, 1996). Mice displayed either hyperplastic nodules progressing to tumors between 11 and 14 months of age (Liang *et al.*, 1996) or induction of metastatic mammary tumors (Jeffers *et al.*, 1998). Consistent with these results, generation of mice expressing HGF under metallothionein control developed tumors of various types, the majority mammary tumors. Together, these studies support a role for HGF in mammary tumor progression.

### Fibroblast growth factors

Early studies with MMTV insertion sites revealed frequent proviral activation of members of the fibroblast growth factor (FGF) family including Fgf3 (Dickson *et al.*, 1984; Peters *et al.*, 1983), Fgf4 (Peters *et al.*, 1989) and Fgf8 (Kapoun and Shackleford, 1997; MacArthur *et al.*, 1995). Direct evidence supporting a role for these growth factors derives from studies of a number of transgenic models. Mammary epithelial expression of Fgf3 (*int2*) results in induction of wide spread mammary epithelial hyperplasias that eventually progress towards full malignancy (Muller *et al.*, 1990). In addition to Fgf3, transgenic mice expressing either Fgf8 (Daphna-Iken *et al.*, 1998) or Fgf7 (Kitsberg and Leder, 1996) under MMTV develop pregnancy-dependent mammary hyperplasias that progress to tumors.

### The role of tumor suppressors in mammary tumor progression

Recent transgenic studies have also highlighted the role of LOH in breast cancer progression. Studies in multiple transgenic mice lines including MMTV/*v-Ha-ras* (Radany *et al.*, 1997), MMTV/wild-type *neu* (Ritland *et al.*, 1997), MMTV/*c-myc* (Weaver *et al.*, 1999) and MMTV/activated *neu* (Cool and Jolicoeur, 1999) have demonstrated that tumors from these animals also show LOH. Significantly, amongst the many areas affected by LOH in these tumors, all showed LOH affecting markers in chromosome 4, an area that contains regions syntenic to human chromosomal regions frequently lost in human breast cancers (1p32-36 and 9p21-22). This further validates these transgenics as models of events involved in human breast cancer. Although it is thought that these LOH mutations affect tumor suppressor genes, many of the loci affected have yet to be identified. However, two types of loss of function mutations that frequently occur in primary human breast cancers are those that affect the known tumor suppressor *p53* and the *BRCA* gene family.

*BRCA1* and *BRCA2* have been strongly implicated in the pathogenesis of familial or heritable breast cancer. In fact, germline mutations in *BRCA1* have been detected in 90% of familial breast/ovarian cancers and almost 50% of familial cases involving breast cancer alone (reviewed in Alberg and Helzlsouer, 1997; Paterson, 1998). The *p53* tumor suppressor has also been frequently investigated, both in the context of breast cancer and cancer in general. In fact, *p53* is the most commonly altered gene by deletion or mutation in human breast cancer (Elledge and Allred, 1994). The advent of gene targeting in embryonic stem cells has enabled researchers to directly assess the importance of both *p53* and the *BRCA* family in mammary tumorigenesis. One problem with this approach is that these mutations either effect viability or life span of the mouse. For instance, mice homozygous for *BRCA1* mutations die early during embryogenesis (Liu *et al.*, 1996). Heterozygotes for *BRCA1* are no more informative as they are not pre-disposed to develop mammary tumors (Liu *et al.*, 1996). Similarly, although mice homozygous for null *p53* do develop a diverse array of tumors, mammary tumors are rarely observed (Donehower *et al.*, 1992). Studies with the *p53* knockouts are further complicated by the formation of extensive lymphomas and thymic tumors that result in the death of the animal at an early age (Donehower *et al.*, 1992). To circumvent these limitations, mice carrying a mutant *p53* 172<sup>Arg-115</sup> under WAP control were generated (Li *et al.*, 1998). These mice display low tumor incidence but exhibit increased tumor incidence as compared to controls in response to chemical carcinogens.

Recent technological advances have also allowed the drawbacks of knockouts, such as embryonic lethality, to be circumvented. Using a powerful modification of the original knockout technique, conditional mutants may be generated which excise the gene of interest in a tissue-specific manner via combination of the Cre-Lox recombination system with the knockin approach. The basis for this system is the ability of the Cre recombinase to excise genetic material flanked by *loxP* sequences from the genome. This can be achieved at the transgenic level through the generation of mice carrying mammary-targeted Cre recombinase under either the MMTV or WAP promoters (for a review of the Cre-Lox system in mice, see Sauer, 1998). These mice are then crossed with mice which have been engineered through homologous recombination techniques to possess *loxP* sequences flanking a critical region of the gene of interest.

This advanced technique has allowed the question of the role of *BRCA* in mammary tumorigenesis to be properly addressed. In the case of the *BRCA1* conditional knockout, Cre-mediated excision of exon 11 of *brca1* in mouse mammary epithelium initially caused increased apoptosis and abnormal ductal development (Xu *et al.*, 1999). Eventually after a long latency, mammary tumors formed which were further associated with genetic instability characterized by aneuploidy, chromosomal rearrangements or alteration of the *p53* locus (Xu *et al.*, 1999), supporting the view that *BRCA1* is involved in DNA repair and maintenance of genomic integrity.

## Transgenic mouse models of multistep carcinogenesis

One of the major lessons the study of these transgenic models has illustrated is that expression of a single activated oncogene or loss of tumor suppressor gene is not sufficient to convert the mammary epithelial cell to the malignant phenotype. To assess the relative contribution of these genetic events to mammary tumorigenesis, investigators have performed genetic crosses between separate transgenic strains harboring these different genetic lesions. One of the first examples of this approach involved the interbreeding of MMTV/*v-Ha-ras* strains with the MMTV/*c-myc* mice (Sinn *et al.*, 1987). In contrast to either parental strain, bi-transgenic mice expressing both *c-myc* and activated *ras* developed focal mammary tumors with a dramatically shortened latency period. Although these experiments demonstrated that *C-myc* and activated *Ras* could cooperate to accelerate mammary tumor formation, both the focal nature of the tumors and the latency period suggested that additional genetic events were required to transform the mammary epithelium to full malignancy.

Another example of this approach is illustrated by crossing the MMTV/*c-myc* strain to mice expressing TGF under MMTV control (Amundadottir *et al.*, 1995). These bi-transgenics exhibited mammary tumors by a mean time of 66 days as compared to 298 days in MMTV/*c-myc* mice. TGF- $\alpha$  mice developed no observable tumors in this study. Significantly, the entire mammary gland was malignant in the bi-transgenics, demonstrating that these two signals are likely sufficient for mammary tumorigenesis to proceed. Interestingly, it appears that both transgenes contribute to mammary epithelial proliferation but TGF- $\alpha$  also acts to prevent *c-myc* induced apoptosis in these tumors (Amundadottir *et al.*, 1995).

Given the ability of EGFR family members to heterodimerize to transduce signals within the cell and the proven importance of Neu and the EGFR ligand TGF- $\alpha$  in mammary tumorigenesis, crosses were generated between transgenics carrying these transgenes under the transcriptional control of MMTV (Muller *et al.*, 1996). Bi-transgenic mice co-expressing TGF $\alpha$  and Neu exhibited accelerated tumor kinetics resulting in multifocal tumors involving the entire mammary gland. In contrast to the parental Neu transgenic strain, mutations could not be detected within the Neu transgene. Conceivably, activation of intrinsic Neu tyrosine kinase activity is achieved in the bi-transgenic tumors by trans-phorylation of Neu by EGFR rather through selection of somatic mutations in the transgene. Interestingly, similar results were obtained in crosses between MMTV/Neu transgenic mice and mice carrying a mutant p53 (*p53 172 R-H*) under WAP control (Li *et al.*, 1997). Again, bi-transgenic mice developed multifocal mammary tumors with a dramatically shorter latency period without evidence of somatic mutations in the transgene. It is possible that inactivation of the p53 tumor suppressor pathway also obviates the selection of activating mutations in the transgene by activating Neu through an independent pathway. In this regard, it is interesting to note that both p53 ablation and TGF- $\alpha$  overexpression are potent anti-apoptotic signals.

Consistent with these studies, inactivation of p53 appears to be a critical event in other transgenic model

systems. For example, mice deficient in p53 have been crossed to a variety of transgenics including MMTV/Wnt1 (Donehower *et al.*, 1995), MMTV/*c-myc* (Elson and Leder, 1995), MMTV/*v-Ha-ras* (Hundley *et al.*, 1997), WAP/IGF-1 (Hadsell *et al.*, 2000) transgenic lines as well as BRCA1 heterozygotes (Cressman *et al.*, 1999) and the conditional BRCA1 knockouts (Xu *et al.*, 1999). With the exception of the MMTV/*c-myc* and MMTV/*v-Ha-ras* strains which died due to extensive lymphomas, inactivation of p53 resulted in a dramatic acceleration of mammary tumor progression. Mammary tumors found in these bi-transgenics also displayed increased aneuploidy as compared to those found in the mono-transgenic alone (Donehower *et al.*, 1995; Hadsell *et al.*, 2000). These results suggest that an absence of p53 predisposes mammary epithelial cells to genetic instability and tumor formation in the presence of some other initiating event such as a growth signal. This necessity for a proliferative signal balanced with an anti-apoptotic is a common theme in many transgenic models. For instance, overexpression of the cell survival factor, Bcl-2, in the mammary glands of WAP/Tag mice also accelerates tumor formation (Furth *et al.*, 1999). Taken together these studies suggest that suppression of apoptotic cell death is a critical step in mammary tumorigenesis in these transgenic models.

## The role of hormones in mammary tumor progression

Many hormones affect the development of the mammary gland and have been tied to breast development and cancer progression. Currently, mouse models exist to address the roles of three of these hormones; prolactin, estrogen, and progesterone. The effects of these hormones on breast cancer have been studied through the use of knockout technologies directed against either their receptors or the hormone itself. Through crosses to established transgenic strains, the contribution of these hormones to the tumorigenesis phenotype is being examined. Together with other lactogenic hormones, prolactin provides signals that drive the development of the mammary gland. Mice lacking the prolactin receptor show defects in mammary gland development with terminal end buds failing to differentiate into proper lobuloalveoli (Briskin *et al.*, 1999). Mice lacking the prolactin hormone itself show arrested mammary gland development. Crosses between the prolactin knockouts and mice expressing the viral oncogene polyomavirus middle T antigen (PyV mT) under MMTV control show slower induced tumor growth than in mice expressing PyV mT alone (Wennbo and Tornell, 2000).

The roles of the steroid hormones estrogen and progesterone in mouse models of breast cancer have both been recently studied. Mice lacking the estrogen receptor alpha, when crossed to MMTV/Wnt1 mice, show greatly decreased tumor kinetics (50%) while having no effect on the formation of early hyperplasias characteristic of the MMTV/Wnt1 strain. Similarly, progesterone receptor function is necessary for mammary gland maturation in normal mammary development (Briskin *et al.*, 1999) as well as for tumorigenesis in a carcinogen-induced mammary tumor model (Lydon *et al.*, 1999). Interestingly, both progesterone



and estrogen have been shown to induce the production of cyclin D1 in murine mammary epithelial cells (Said *et al.*, 1997). These results indicate that hormonal effects may play an important role in mammary cancer progression. Further studies using a wider number of established models should greatly increase our knowledge of their precise roles and effects.

One of the primary limitations to many of these transgenic models discussed is their dependency on strong viral, hormonally sensitive promoters such as WAP and MMTV. Consequently, it is difficult to properly address the interactions between the oncogene-coupled signaling pathways and endocrine hormones that affect mammary gland development. This problem is being addressed by the use of knockins in which transgenics are generated which express oncogenes of interest from their endogenous promoters. This is achieved through the use of a modified homologous recombination approach by which oncogenes of interest are introduced into their endogenous loci.

A combination of both tissue specific recombination and knock-in technologies has enabled researchers in this lab to place the activated *neu* under the endogenous *erbB-2* promoter (Andrechek *et al.*, 2000). To prevent the early embryonic lethality that may have resulted from expression of this cDNA, a silencer cassette containing a neo cassette flanked with *loxP* sites was placed between the *erbB-2* promoter and the activated *neu* allele. This resulted in expression of the endogenous ErbB-2 until the silencer cassette was excised by mammary epithelial specific expression of the Cre recombinase resulting in mammary epithelial specific expression of the activated ErbB-2 allele (Andrechek *et al.*, 2000). Expression of this allele in the mammary gland resulted in accelerated lobuloalveolar development and tumor formation after a long latency period (Andrechek *et al.*, 2000). Significantly, normal levels of expression of the activated allele from the endogenous *erbB-2* promoter were not sufficient for tumorigenesis as all tumors showed amplification (2–22 copies) of the activated *neu* allele relative to normal mammary tissue (Andrechek *et al.*, 2000). Thus like ErbB-2 positive human tumors, mammary tumorigen-

esis in this mouse model required amplification of the *erbB-2* locus. This model thus holds great promise for relevant studies of the pathogenesis of ErbB-2 positive human breast cancer.

## Conclusions

It is evident from the models outlined above that it is important to consider many factors when assessing the applicability of a mouse model for breast cancer research to human breast cancer. The nature of the genetic change, the characteristics of the promoter used to target transgene expression, the status of endogenous signaling pathways, the spectrum of additional mutations that may arise during tumor progression in the transgenic, the number of transgenic lines examined and the reliability of the phenotype amongst them, the transgenic's genetic background and the molecular pathology and histology are all important indicators of the relevancy of the model to the human disease.

While no single genetically engineered mouse can offer a complete model of the wide assortment of human neoplasms found in human breast cancer, it is hoped that these multiple approaches will enable us to develop insights into the complex molecular events involved in tumorigenic progression of the breast. One common theme evident from these studies is the involvement of genes necessary for normal mammary gland development in the progression of this disease. Another emergent theme is the complex, multi-step nature of all stages of breast cancer progression from initial tumor formation to final metastasis. Fortunately, researchers now have many models available to them to study these steps in a controlled and rational manner. Furthermore these models provide the opportunity to study many various aspects of the pathogenesis of this disease, from hormonal effects to responses to chemotherapeutic drugs. It is hoped that through the combined use of these models, and the further development of more relevant models that a deeper understanding of this disease and the generation of new therapeutic agents will result.

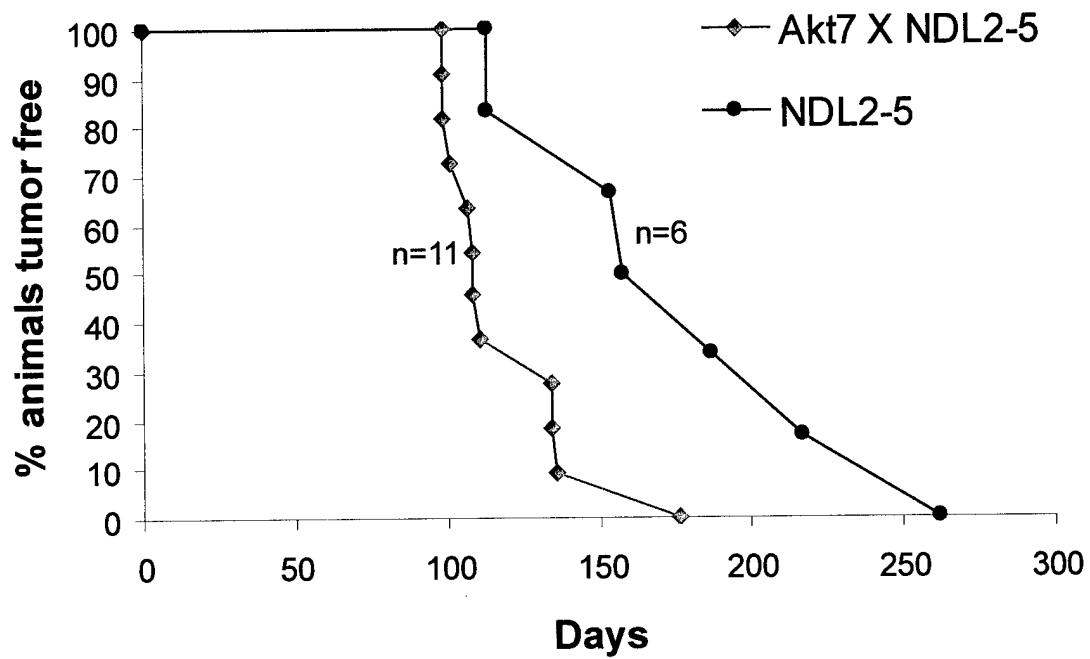
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**Appendix 2**  
Figures



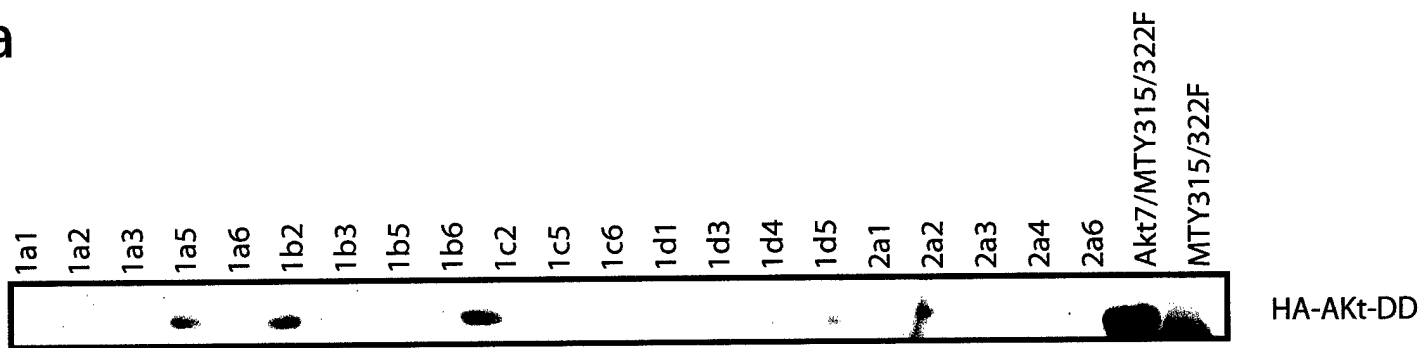
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## Figure 1

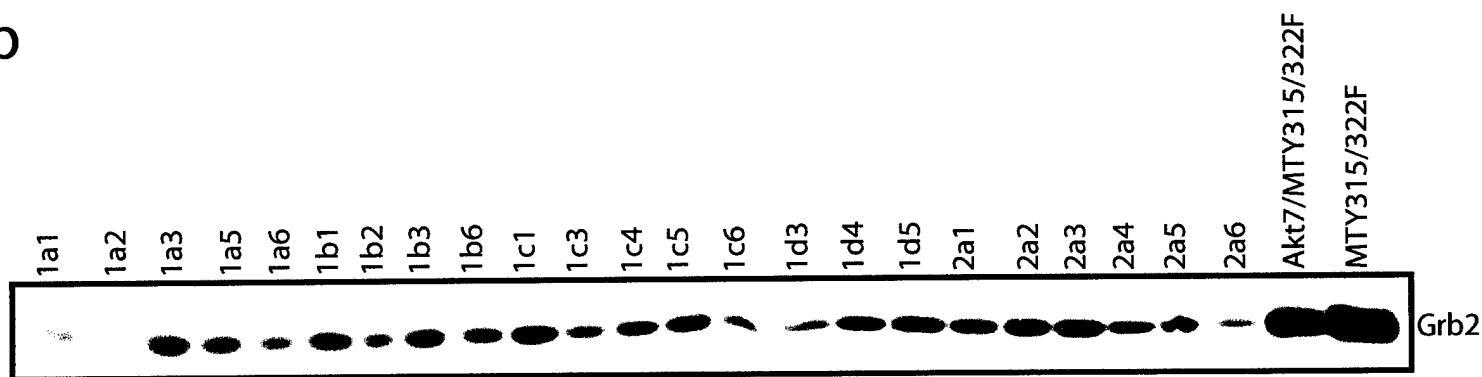
### **Mammary tumor kinetics in transgenic strains.**

Mammary tumor kinetics of MMTV/NDL2-5 (n=6) and MMTV/Akt7 X MMTV/NDL2-5 (n=11) strains. The age indicated is that at which a mammary tumor is first palpable in each transgenic strain.

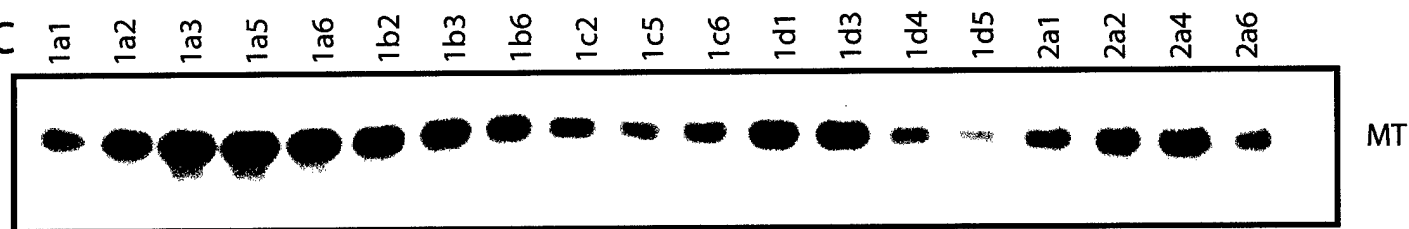
a



b



c

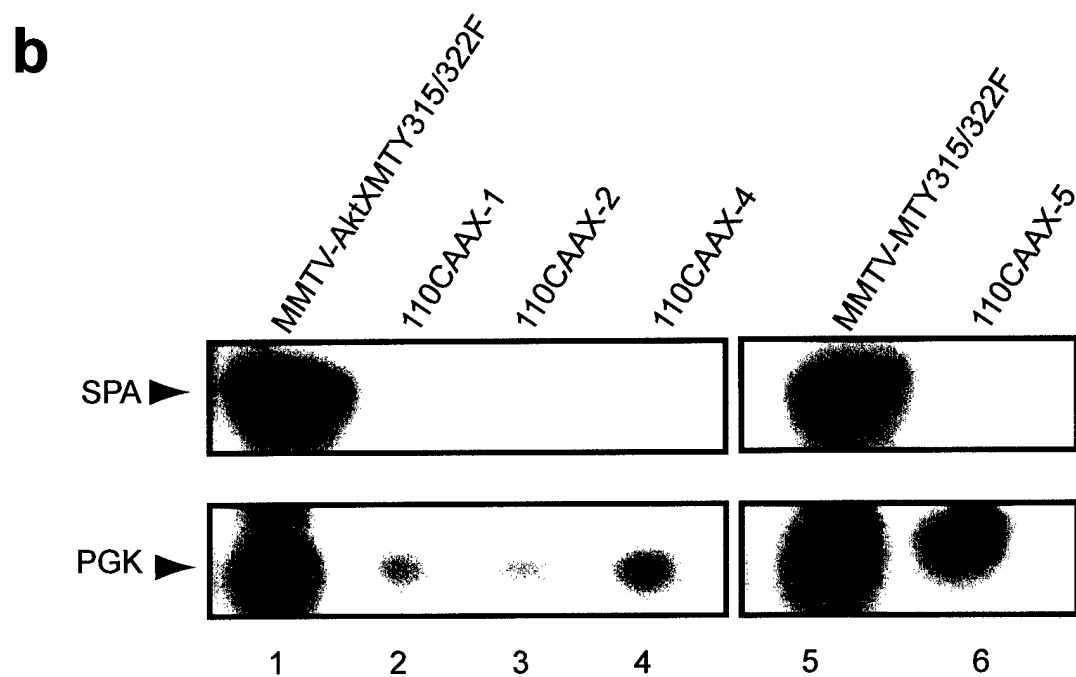
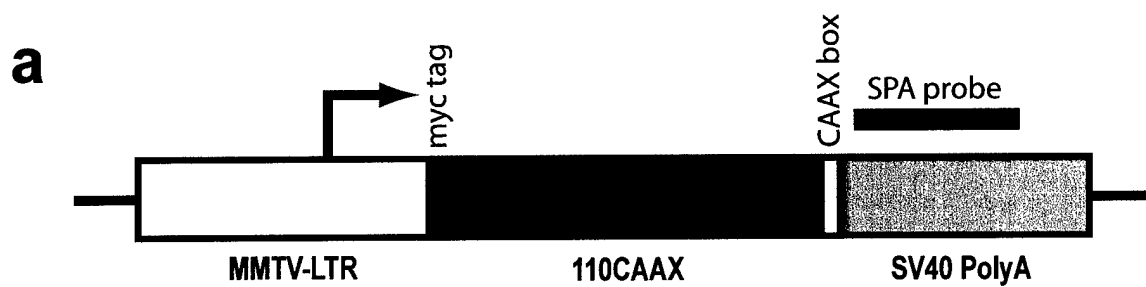


## Figure 2

### Transgene expression in AktXMTY315/322F cell lines

- a) Immunoblot analysis of expression of HA-Akt-DD in AktXMTY315/322F cell lines. Fifty micrograms of total protein lysate was subjected to anti-HA immunoblot analysis with HA-11 monoclonal antibody (Babco).
- b) Immunoblot analysis of expression of Grb-2 (loading control) in AktXMTY315/322F cell lines.
- c) RNase protection analysis of expression of MTY315/322F in AktXMTY315/322F using a probe directed against the MT transgene.





**c**

Line	Expression
110CAAX-1	—
110CAAX-2	—
110CAAX-4	—
110CAAX-5	—

### Figure 3

#### **Activated PI3K transgenic construct and expression.**

- (a) Structure of the MMTV/110CAAXkt transgene. The Bluescript vector backbone is represented by a thin line on either side of the expression cassette, with the large white region corresponding to the MMTV LTR derived from plasmid pAp, the black portion corresponding to the myc tag, the dark grey region corresponding to the PI3K (p110CAAX) cDNA, the small white region corresponding to the ras-derived CAAX motif, and the mid-grey region corresponding to the transcriptional processing sequences derived from the SV40 early transcription unit. Also shown is the antisense probe and its position within the SV40 polyadenylation sequences. The transcription start site is indicated by the arrow.
- (b) **Transgene expression in MMTV/110CAAX transgenic mice**  
RNA transcripts corresponding to the 110CAAX transgene in various 110CAAX transgenic strains. Total RNA (30 ug) was derved from mammary glands of virgin female. The antisense probe used in this analysis protects a 285 bp fragment corresponding to the SV40 polyadenylation signals on the 110CAAX transcript. Also shown are postive control samples derived from MMTV-Akt7XMTY315/322F and MMTV/MTY315/322F transgenics.
- (c) **Summary of 110CAAX expression data.** The 110CAAX-3 line was not examined as it failed to pass the transgene.

**Appendix 3**

Abstracts from conferences

Activation of Akt/PKB in mammary epithelium interferes with mammary gland involution and provides a critical cell survival signal required for tumor progression.

**John Hutchinson BSc<sup>1</sup>, Jing Jin PhD<sup>2</sup>, Robert D. Cardiff MD, PhD<sup>3</sup>, Jim R. Woodgett PhD<sup>2</sup> & William J. Muller PhD<sup>1</sup>**

<sup>1</sup> MOBIX, McMaster University, Hamilton, Ontario, Canada

<sup>2</sup> Ontario Cancer Institute, Toronto, Ontario, Canada

<sup>3</sup> University of California at Davis, Davis, California, USA

The mammary gland undergoes a regulated cycle of proliferation, differentiation and apoptosis and disruption of this cycle can lead to the occurrence of many abnormalities including tumorigenesis. In conjunction with hormones and cell-substratum interactions, the growth, differentiation and apoptosis of mammary epithelial cells is regulated by growth factors and their receptors. Activation of these receptors leads to the recruitment of a number of cytoplasmic signaling molecules including the phosphatidylinositol 3 $\alpha$ -OH kinase (PI3K) which plays an important role in coupling these growth factor receptors to cell survival pathways via the Akt/PKB (Protein Kinase B) serine/threonine kinase. Evidence supporting the importance of the PI3K/Akt signaling pathway in mammary tumorigenesis stems from experiments with transgenic mice bearing polyomavirus middle T antigen (PyV mT) under the control of the mouse mammary tumor virus-long terminal repeat promoter (MMTV-LTR). Mammary epithelial specific-expression of PyV mT results in the rapid development of multifocal metastatic mammary tumors whereas transgenic mice expressing a mutant mT de-coupled from the phosphatidylinositol 3 $\alpha$ -OH kinase (MTY315/322F) develop extensive mammary gland hyperplasias that are highly apoptotic. To directly assess the role of Akt in mammary epithelial development and tumorigenesis, we generated transgenic mice expressing constitutively active Akt (Akt-DD). Although expression of Akt-DD interferes with normal mammary gland involution, tumors were not observed in these strains. However, co-expression of Akt-DD with MTY315/322F resulted in a dramatic acceleration of mammary tumorigenesis correlated with reduced apoptotic cell death. Importantly, we did not observe an associated restoration of wildtype metastasis levels in the bi-transgenic strain. Taken together these observations indicate that activation of Akt can contribute to tumor progression by providing an important cell survival signal but does not promote metastatic progression.

Activation of Akt/PKB in mammary epithelium interferes with mammary gland involution and provides a critical cell survival signal required for tumor progression.

**HUTCHINSON JN, JIN J, CARDIFF RD, WOODGETT JR & MULLER WJ.**  
**McMaster University, Hamilton, ON, Canada.**

The mammary gland undergoes a regulated cycle of proliferation, differentiation and apoptosis and disruption of this cycle can lead to the occurrence of many abnormalities including tumorigenesis. In conjunction with hormones and cell-substratum interactions, the growth, differentiation and apoptosis of mammary epithelial cells is regulated by growth factors and their receptors. Activation of these receptors leads to the recruitment of a number of cytoplasmic signaling molecules including the phosphatidylinositol 3'-OH kinase (PI3K) which plays an important role in coupling these growth factor receptors to cell survival pathways via the Akt/PKB (Protein Kinase B) serine/threonine kinase. Evidence supporting the importance of the PI3K/Akt signaling pathway in mammary tumorigenesis stems from experiments with transgenic mice bearing polyomavirus middle T antigen under the control of the mouse mammary tumor virus-long terminal repeat promoter (MMTV-LTR). Mammary epithelial specific-expression of polyomavirus middle T antigen results in the rapid development of multifocal metastatic mammary tumors whereas transgenic mice expressing a mutant middle T antigen de-coupled from the phosphatidylinositol 3'-OH kinase (MTY315/322F) develop extensive mammary gland hyperplasias that are highly apoptotic. To directly assess the role of Akt in mammary epithelial development and tumorigenesis, we generated transgenic mice expressing constitutively active Akt (Akt-DD). Although expression of Akt-DD interferes with normal mammary gland involution, tumors were not observed in these strains. However, co-expression of Akt-DD with MTY315/322F resulted in a dramatic acceleration of mammary tumorigenesis correlated with reduced apoptotic cell death. Furthermore, co-expression of Akt-DD with MTY315/322F resulted in phosphorylation of the FKHR forkhead transcription factor and translational upregulation of cyclin D1 levels. Importantly, we did not observe an associated restoration of wildtype metastasis levels in the bi-transgenic strain. Taken together these observations indicate that activation of Akt can contribute to tumor progression by providing an important cell survival signal but does not promote metastatic progression.

# Mammary Epithelial Expression Of Akt/Pkb Affects Mammary Gland Involution And Tumor Progression.

**John Hutchinson<sup>1</sup>, Jin Jing<sup>2</sup>, Robert Cardiff<sup>3</sup>, Jim Woodgett<sup>2</sup> & William Muller<sup>1</sup>.**

**<sup>1</sup>McMaster University, Hamilton, ON, Canada; <sup>2</sup>Ontario Cancer Institute, Toronto, ON, Canada; <sup>3</sup>University of California at Davis, Davis, California, USA.**

In conjunction with hormones and cell-substratum interactions, the growth and differentiation of mammary epithelial cells is regulated by growth factors and their receptors. Activation of these receptors leads to the recruitment of a number of cytoplasmic signaling molecules to the cell membrane including the phosphatidylinositol 3 $\alpha$ -OH kinase (PI3K). Recruitment and activation of PI3K by these docking molecules results in the activation of a number of Peckstrin homology domain harbouring molecules including the Akt serine/threonine kinase. Akt plays roles in coupling these receptors to critical cell survival pathways through inhibition of pro-apoptotic signals from BAD, caspase-9 and the forkhead transcription factor family as well as the promotion of survival signals from NF $\kappa$ -B. Although evidence suggests roles for the PI3K and Akt/PKB in normal mammary development and tumorigenesis there is no direct evidence tying them to these processes in the mammary gland. To assess the role of Akt in mammary epithelial development and tumorigenesis, we generated transgenic mice expressing activated Akt in the mammary epithelium. Although Akt interferes with the normal apoptotic process of mammary gland involution, mammary tumors were not observed in this strain after more than a year of observation. However, co-expression of activated Akt with a mutant form of Polyomavirus middle T (PyV mT) antigen de-coupled from the PI3K signaling pathway results in a dramatic acceleration of mammary tumorigenesis in this strain. This acceleration was further correlated with reduced apoptotic cell death in mammary epithelium expressing the mutant form of PyV mT. Importantly, associated wildtype PyV mT levels were not observed. These observations suggest that activation of Akt can contribute to tumor progression by providing a cell survival signal but that Akt/PKB does not contribute to metastasis.